#### ST,C-Biotech/ChemLib

From:	7
Sent: \ To:	
Subject:	u

Chan, Christina

Tuesday, January 21, 2003 12:07 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/767215

#### Please rush. Thanks Chris

Chris Chan ,TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

Proty date 2/2000

----Original Message----From: Davis, Minh-Tam

Sent: Tuesday, January 21, 2003 11:58 AM

Chan, Christina To:

Subject: Rush search request for 09/767215

Please search in commercial database and in issued patent files:

1) Oligomer search for SEQ ID NO:2.

2) Amino acids 10-116, 126-420, 568-660, 676-745, 826-1004 of SEQ ID NO:2.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

**Edward Hart** Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203 fd nothig Heat is even 25 aa as pui art

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e= "Tyrosine kinase phosphorylation site"
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                                                                  The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bci-10 and stimulates phosphorylation of Bci-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., cyndromes), myocardial infarctions, strokes, immune disorders (e.g., cyndromes).
regulating growth and cell death and useful for the treatment of cancer
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VNSYTMKDTAAHGIIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAK 780

YKRLLQDLEAKVATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHR 720

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Human; caspase recruitment domain-14; CARD-14; chromosome 17; nuclear factor-kappa B; NE-kB; cell growth; cell death; cancer; therapy; autoimmune disorder; systemic lupus erythematosus; neurological disorder; Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia haematological disorder; myelodysplastic syndrome; myocardial infarction; stroke; immune disorder; Crohn's disease; allergic rhinitis; infection; cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autolimnum disorders (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                        ALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                               predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                            DRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by TGG"
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                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    AAE07165 standard; Protein; 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001; 2001WO-US02087
                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                    AAE07165;
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(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                             treatment.
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                                                                                                                                                                                                                                                               RESULT
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systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., ameamia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
                                                                                                                                                                                                                                                                                          792
                                                                                                                                                                                              852
                                                                                                                                                                                                                            TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDGYKRLLQDLEAKV 672
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                 LHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAP
                                                                                            SGVLMRRRPARRILSQVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPG
                                                                                                                                   GTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAKASPLRLSFDRGQ
                                                                                                                                                                                                                     LDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRPVLLVPRAVGKILSEKLCLLQGFK
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0
                                                              Length 1139;
                                                                              1; Indels
                                                              DB 22;
                                                              Score 343; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Human EST encoded protein SEQ ID NO: 1927.
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                                                                                                                                                                                                                                                                                                                        1023 DGWSDLDGLLSCVRQAIADEQKKV 1046
                                                                                                                                                                                                                                                                                                                DGWSDLDGLLSCVRQAIADEQKKV 996
                                                                                                                                                                                                                                                                                                                                                                    AAM24402 standard; Protein; 148
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2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                               34.2%;
Local Similarity 99.8%;
les 443; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                 1139 AA;
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17-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                 Sequence
                                                                 Query Match
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Matches
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, foremaics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ü
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                                                                                                                                                  Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
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Asundi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 10; DB 22; Length 148; 100.0%; Pred. No. 0.44; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pilarsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate tumor EST fragment derived protein #39.
  Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt A,
     ,2
        Wang
                                Zhang J, Werhman T;
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                                                                                                                                                                                                                                   Claim 20; Page 1236; 1275pp; English.
        Qian XB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY73852 standard; Protein; 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98DE-1020190.
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          Zhou
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Best Local Similarity
Matches 10; Conservat
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N-PSDB; AAZ52870.
     Tang YT, Liu C, Zhk
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 RPARPRPVLL 832
                                                                                 WPI; 2001-476164/51
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                                                                                                            N-PSDB; AAH99061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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to the sample; and (3) detecting a decrease in formaldehyde in the sample. A biosensor and bioremediation system for environmental
                                     formaldehyde are obtained.
                                                                                Sequence
                                                                                                                                                                                                                                                                                                                       AAU30127
ID AAU
                                                                                                                                                                                                                                                                                                       RESULT 6
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library derived expressed sequence tag (EST) sequences represented in AAZ52858-253014.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting and remediating formaldehyde. A claimed method for oxidizing formaldehyde in a sample involves: (1) providing R. sphaeroides cells that comprise a glutathione-dependent formaldehyde dehydrogense (GSH-FDH) gene, especially the R. sphaeroides adhl gene (see AAF90615), an adhl promoter operably linked to the GSH-FDH gene, a cis-acting operator, at least 1 protein that senses formaldehyde (especially Gfds and GfdT), and a protein that senses formaldehyde (especially Gfds and GfdT), and a trans-acting regulatory protein (especially GfdR) that modulates trans-acting regulatory protein (especially GfdR) that modulates formaldehyde sensor protein(s), such that the promoter and operator together specifically direct transcription of the GSH-FDH gene in response to a signal from the together specifically direct transcription of the GSH-FDH gene when the cell is exposed to formaldehyde; (2) adding the bacterial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gidr encoded by an open reading from of the formaldehyde-inducible regulatory system (see AAF90616) of Rhodobacter sphaeroides. Hydropathy analysis of the sequence suggests Gidr to be a transmembrane protein. A second open reading frame encodes Gids (see AAB82497), a putative soluble protein. By analogy to other systems, it is thought that a His residue near the C-terminal end of Gids may be dephosphorylated when formaldehyde binds to Gidr. In the absence of formaldehyde, the phosphate on Gids may be transferred to an Asp residue of the repressor GidR (see AAB82495). These proteins are utilised in methods of the invention for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the formaldehyde sensor protein
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                                                                                            Score 10; DB 20; Length 229;
Pred. No. 0.65;
                                                                                                                                         0; Indels
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                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                       AAB82496 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Formaldehyde sensor protein GfdT.
                                                                                                         100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Formaldehyde dehydrogenase;
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97US-0919953.
                                                                                                1.0%;
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                                                                                                                   Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter sphaeroides
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77 RPARPRPVLL 86
                                                        229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF90616
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                                                           Sequence
                                                                                                Query Match
                                                                                                                                                                                                                                                                                  RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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   22; Length 390;
                                                                0; Indels
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      DB 22
1.1;
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                                                                   Mismatches
   Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 AAU30127 standard; Protein; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 247; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #618.
                                                                ;
0
                              100.08;
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26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac
Query Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611725/70.
                                                                                                                                308 LRERAVAAER 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200179449-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-2001
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Protein #4316 encoded by probe for measuring heart cell gene expression.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                               claim 27; SEQ ID NO 29638; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene expression, heart; microarray, vascular system, cardiovascular disease, hypertension, cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9;
Pred. No.
                                                                                                                                                                                                                                               Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB22317 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Sco...
100.0%; Pre
                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-024263
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                                                                     30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease.
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                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                         WPI; 2001-483447/52
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tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 AA;
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            WO200157277-A2
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                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                               26-MAY-2000;
30-JUN-2000;
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                                        09-AUG-2001
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                                                                                                                                                                                                                                               Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR51227 showes the antigen peptide for a monoclonal antibody having immobility action of human sperm and inhibitory action of fertilisation. It is useful for a contraception vaccine and for the
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - used in
                                                                                                                                                                                                                                                                                                                                                /label- membrane antigen peptide of human sperm
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                                                                                                                                                                                                                                               Membrane antigen peptide; human sperm; contraceptive vaccine; diagnosis of infertility; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane antigen peptide of human sperm and its coding -
a contraceptive vaccine and for diagnosis of infertility
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0
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 Mismatches
                                                                                                                                                                                                                    Membrane antigen peptide of human sperm
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..335
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                                                                                                                              AAR51227 standard; Protein; 334 AA.
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                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-128676/16.
N-PSDB; AAQ45175.
                                             PDVDFSNFSG 117
                            PDVDFSNFSG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOJ/) ISOJIMA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1992;
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1992;
                                                                                                                                                                                        23-NOV-1994
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 10;
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Matches
   Matches
                            108
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                                                                                                   RESULT 7
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Gaps

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Length 348; 0; Indels

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WPI; 2001-483446/52.
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21-SEP-2000; 2
27-SEP-2000; 2
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                    microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                              AAM70143;
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                                                                            Query Match
                       Single
                                                                                                                                                                                                                                                                                                                                                                         Human;
                                brains
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                   The present invention relates to single exon nucleic acid probes for ameasuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, human standon, cardiac arritythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 29835
                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                           Length 348;
                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                           Score 9; DB 22;
Pred. No. 9.1;
Mismatches
                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                  Claim 15; SEQ ID No 24087; 530pp; English
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                                                             Rank DR;
                                                                                                                                                                                                                                                                                                            0.9%; Score 9;
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                                                                                                                                                                                                                                                                                                           0.9%;
100.0%; Pic
0;
                                         (MOLE-) MOLECULAR DYNAMICS INC
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                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK, Chen W,
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
9; Conserve
                                                                              WPI; 2001-488899/53
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224 RLKEENEKL 232
                                                                                                                                                                                                                                                                                                                                                    266 RLKEENEKL 274
                                                                                                                                                                                                                                                                                         348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epilepsy; cancer.
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                          Sednence
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                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                     The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone marrow expressed exon; gene expression analysis; probe; rray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                           Example 4; SEQ ID NO: 29835; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 9; DB 22;
100.0%; Pred. No. 9.1;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53.
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224 RLKEENEKL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                      348 AA;
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Peptide #4518 encoded by probe for measuring placental gene expression.
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                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human placenta
                                   AAM30481 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                                                                                                                                                                            DK,
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es 9; Conserv
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                                                                                                                                                                              Homo sapiens
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                                                             AAM30481;
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AAM05610
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          RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SEMP: see AAIIO08-AAIIS4659). The present sequence is a peptide encoded by one such probe. The SEMPS are derived from human HeLa cells. The SEMPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                         Peptide #4409 encoded by probe for measuring cervical gene expression.
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                                                  Gaps
                                                                                                                                                                                                                                                                 human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
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                       Length 348;
                                                 0; Indels
                       DB 22;
5. 9.1;
                                                 Mismatches
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                                      Pred. No.
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                      Query Match 0.9%; Score 9; Best Local Similarity 100.0%; Pred. No Matches 9; Conservative 0; Mismatch
                                                                                                                                                                AAM17975 standard; Protein; 348 AA.
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26-MAY-2000; 2000US-0207456.
30-UNN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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Best Local Similarity
9; Conserve
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224 RLKEENEKL 232
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348 AA;
                                                                                                                                                                                                                                                                                 cervical cancer
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                                                                                                                                                                                                                                                                                                         Homo sapiens.
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  Sednence
                                                                                                                                                                                                                                                                    Probe;
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Rank DR

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                                  The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
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                                                                                                                                                                                                                       Length 348;
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100.0%; Pred. No. 9.1
ive 0; Mismatches
Claim 27; SEQ ID No 30750; 654pp; English.
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WO200186003-A2.
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                                                                                                                                                                                                                                                                                    The present invention relates to novel single exon nucleic acid probes (see AA10010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognesing predicting, diagnosing, grading, staging, monitoring and prognesing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human peptide encoded by genome-derived single exon probe SEQ ID 29447.
                                                                                                                                                                                                                                 Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histocytosis; lymphangiolejomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          breast disease and non-carcinoma tumours
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100.0%; Pre
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                                                                                                                   21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                     29-JAN-2001; 2001WO-US00661.
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224 RLKEENEKL 232
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                                                                                                                                                                                                                                             in a human breast
         WO200157270-A2
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uncleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 15614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the array; identifying exons in a eukaryotic genome, comprising (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences of the above mentioned microarray; assigning exons to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes of probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (LDD), interstitial lung disease (LDD), family and a sathmin Plots disease (LDD), family and analysis, publicas, Harmania of expression and probably and a sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spatially-addressable \ set \ of \ single \ exon \ nucleic \ acid \ probes, \ used \ to \ measure \ gene \ expression \ in \ human \ lung \ samples \ -
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Pred. No. 9.1;
Mismatches
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2000US-0608408.
2000US-0632366.
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2000US-236359P.
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15-NOV-2001
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266 RLKEENEKL 274

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CITY: King of Prussia
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Sequence 6, Appli
Sequence 2, Appli
Sequence 188, App
Sequence 188, App
Sequence 188, App
Sequence 188, App
Sequence 118, App
Sequence 11, Appl
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1554.769 Million cell updates/sec
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1 MGELCRRDSALTALDEETLW.....VRQAIADEQKKVVWTEQSPR 1004
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-874-118-6
US-08-747-116-2
US-08-747-116-2
US-08-951-843A-188
US-08-954-549A-307
US-08-954-549A-307
US-08-955-111
US-09-395-689-3
US-09-395-689-3
US-09-154-750A-79
US-09-154-750A-79
US-09-154-750A-13
US-08-765-551-13
US-08-765-551-13
US-08-765-751-13
US-08-761-761-761-13
US-09-231-529-1
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US-09-100-664A-4
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                                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                        January 22, 2003, 08:58:25
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Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Match I
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Maximum DB
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RESULT 1
US-09-192-983-5
Sequence 5, Application US/09192983A
Sequence 5, Application US/09192983A
Patent No. 6242244
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296.95505
CURRENT FAPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/6919,953
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1996-02-28
SOFWWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 390
TYPE: PRT
CORGANISM: Rhodobacter sphaeroides
US-09-192-983-5
   Sedinence Sedine
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Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                     US-09-335-983-3
US-09-335-983-4
US-09-155-083-2
US-09-320-535-2
US-09-320-535-9
US-09-155-036-22
US-09-155-036-23
US-09-155-036-24
US-09-155-036-26
US-09-137-077-2
US-09-135-036-5
US-09-135-036-5
US-09-135-036-5
US-09-155-036-5
US-09-155-036-5
US-09-155-036-5
US-09-155-036-5
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0.32;
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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100.0%; Pred. No. 0.3
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,941
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 8; DB 4;
100.0%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GMLO'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/08879941; Patent No. 6268172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 446 amino acids
amino acid
                                                      INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
                                                                                                                                                           ; TOPOLOGY: linear
US-08-874-138-6
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220 LQEELNQE 227
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US-08-879-941-2
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                                                                                                             COMPUTER: 148 COMPADIATE
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY-AGENT INFORMATION:
NAME: Gimmi, EGWART R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 950475
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8%; Score 8; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANN: Wallis, Nicola
TITLE OF INVENTION: No. 5882889el Compounds
WIMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: GM10015
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08874138 Patent No. 5882889
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 326:
                    COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-326
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
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US-08-874-138-6
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 24;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 7; DB 3;
100.0%; Pred. No. 20;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015389-002930US
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
                                                                                                        APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/974,549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 307, Application US/08974549A Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGIETRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 180
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Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                            FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-974-549A-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-851-843A-188
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                                                                              APPLICANT: Wallis, Nicola
TITLE OF INVENTION: NOVEL HISTIDINE KINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6093809el Telomerase NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/747,116
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
WENTION: No. 6093809el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 8; DB 4
100.0%; Pred. No. 31;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 188, Application US/08851843A Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GM10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,941
FILING DATE:
                     Sequence 2, Application US/09747116
Patent No. 6348340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
                                                                                                                                                                                                                                                  COUNTRI.

ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: DISKETTE
MEDIUM TYPE: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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TOPOLOGY: linear
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Best Local Similarity
                                                               GENERAL INFORMATION:
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220 LQEELNQE 227
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  US-09-747-116-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DGCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 7; DB 4
100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: 390
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION 536
PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 188, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 24 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-854-050-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       759 TRKPSSG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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US-09-430-323-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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APPLICANT: Cech, Thomas R.
APPLICANT: Cach, Thomas R.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Maxim. Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 7; DB 4;
100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 307:
                                                                                                                                  PFILING DATE:

APPLICATION DATA:

APPLICATION NUMBER:

BFILING DATE:

APPLICATION NUMBER:

BFILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

BFILING DATE:

APPLICATION NUMBER:

BFILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRICH APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRICH APPLICATION NUMBER:

APPLICATIO
                                             CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 188, Application US/08854050 Patent No. 6261836
   FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-974-549A-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   759 TRKPSSG 765
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## Sequence 3, Application

## Sequence 3, Application

## APPLICANT: Hwang, Jaulang

## APPLICANT: Chen, Tacing Yueh

## TITLE OF INVENTION: TOPOISOMERASE 1-MEDIATED DNA DELIVERY

## TITLE OF INVENTION: TOPOISOMERASE 1-MEDIATED DNA DELIVERY

## TITLE OF INVENTION: TOPOISOMERASE 1-MEDIATED DNA DELIVERY

## CURRENT APPLICATION NUMBER: US/09/395,689

## CURRENT FILING DATE: 1999-09-13

## NUMBER OF SEQ ID NOS: 6

## SOFTWARE: FastSEQ for Windows Version 4.0

## SEQ ID NO 3

## LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
APLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPERENCE: UTSW0708
CURRENT APPLICATION UNMER: US/09/562,737
CURRENT FILING DATE: 200-05-01
NUMBER OF SEQ ID NOS: 132
                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 126, Application US/09562737 Patent No. 6428967 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0./v,
100.0%; Pr
                                          NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34028
REFERENCE/DOCKET NUMBER: 9501
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 270-5024
TELEFAX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Sc
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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US-09-395-689-3
                      ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrev A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                            ; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US94-06655-11
                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 7; Conser
  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: human US-09-562-737-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-562-737-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Pa
SEQ ID NO 126
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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0
                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Lam PC compatible
COMPUTER: Talm PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION ONNBER: US 08/854,050
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chaiken, Irwin
APPLICANT: Graddis, Thomas
APPLICANT: Myszka, David
TTLE OK INVENTION: Coiled-Coil Stem Loop Templates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: SMITHKINE Beecham Corporation
STREET: Corporate Patents / P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

RECISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 188:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 20; Matches 7; Conservative 0; Mismatches
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-430-323-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US94-06655-11; Sequence 11, Application PC/TUS9406655; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 24 amino acids
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                                                                                                                                                                       CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTORNEY AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                           OFEWATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
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100.0%; Pred. No. 97;
ive 0; Mismatches
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Sequence 79, Application US/09154750A

GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: MINALEr, Kenneth
FILE REFERENCE: 1107-75357
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 06/059,153
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-183
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 136
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Pred. No.
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v 100.0%; Pre
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                       136 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-154-750A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Matches 7; Conserv
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: WORG, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
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  Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                        0; Indels
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Fatent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Paul W. Zimmerman ADDRESSEE: Paul W. Zimmerman ADDRESSEE: Intellectual Property Services ADDRESSEE: Battelle Memorial Institute ADDRESSEE: PNNL P.O. Box 999
STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
ZIR: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
0.7%; Score 7; DB 4;
100.0%; Pred. No. 76;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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FILING DATE: Unknown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                              Sequence 36, Application US/08853659A Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                Best Local Similarity 100.
Matches 7; Conservative
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                                                                             268 KEENEKL 274
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58 KEENEKL 64
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US-08-853-659A-36
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US-08-946-914-13
    Query Match
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LENGTH: 1004
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Sequence 16, Appl
Sequence 18, Appl
Sequence 37615, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 188, App
Sequence 37819, A
Sequence 35935, A
Sequence 35935, A
Sequence 35935, A
Sequence 5287, Ap
Sequence 5287, Ap
Sequence 10, Appl
Sequence 13, Appli
Sequence 13, Appli
Sequence 26, Appli
                                                                                   2003, 08:57:45 ; Search time 14 Seconds (without alignments) 1447.090 Million cell updates/sec
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                                                                                                                                                                              1 MGELCRRDSALTALDEETLW......VRQAIADEQKKVVWTEQSPR 1004
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
5.1.3
Compugen Ltd
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US-10-032-159A-18

US-09-864-761-37615

US-09-843-66-188

US-09-438-486-188

US-09-438-486-188

US-09-864-761-35935

US-09-864-761-35935

US-09-864-761-33346

US-09-138-626-5287

US-09-138-626-5287

US-09-138-626-5287

US-09-138-626-5287

US-09-138-626-5287

US-09-138-626-5287

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US-09-138-626-5287
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US-09-263-689-13
US-09-866-582-26
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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US-09-767-215-5
                                                                                                                                                                                                                                                       122226 seqs, 20178551 residues
GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                           - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length
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Perfect score:
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Sequence 210, Appl Sequence 13, Appl Sequence 1468, App Sequence 326, Appl Sequence 1, Appl Sequence 1, Appl Sequence 20, Appl Sequence 2, Appl Sequence 14, Appl Sequence 19, App Sequence 219, App Sequence 243, App Sequence 399, App Sequence 98, Appl Sequence 100, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 102, App Sequence 103, App Sequence 101, App Sequence 103, App Sequence 103, App Sequence 103, App Sequence 101, App Sequence 103, App Sequence 104, App Sequence 105, App Sequence 105, App Sequence 105, App Sequence 106,	
9 US-10-001-876-210 10 US-09-767-041-13 10 US-09-225-300-1468 110 US-09-225-300-1468 120 US-09-880-192-62 130 US-09-981-1326 140 US-09-931-381A-2 150 US-09-931-381A-2 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-381A-3 150 US-09-931-399 150 US-09-930-93 150 US-09-930-93 150 US-09-796-990-93 150 US-09-796-990-101 150 US-09-796-990-102 150 US-09-796-990-103 150 US-09-796-990-103	
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## ALIGNMENTS

61 PRLTNSAMRAGHLLDLLKTRGKNGALAFLESLKFHNPDVYTLVTGLQPDVDFSNFSGLME 120 121 TSKLTECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRM 180 241 SCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE 300 Gaps 1 HILLING THE STATE THE ST 181 KREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVS 1 MGELCRRDSALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHS .; Length 1004; Sequence 2, Application US/09767215

Patent No. US20020081636A1

GENERAL INFORMATION:

APPLICANT BETLIO, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-142001

CURRENT APPLICATION NUMBER: US/09/767,215

PRIOR PAPLICATION NUMBER: 001-01-22

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0 Indels DB 10; Mismatches Score 1004; Pred. No. 0; 0 100.08; 100.08; Ouery Match Best Local Similarity 100. Matches 1004; Conservative TYPE: PRT ORGANISM: Homo sapiens US-09-767-215-2

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LVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKE
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
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CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
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SOFTWARE: FastSEQ for Windows Version
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                                      Gaps
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                                    Indels
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APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

FILE REFERENCE: P-LJ 5100

CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2000-12-19

PRIOR PILING DATE: 2000-12-21
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Pred. No. 1.6e-104;
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 Score 343;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                  Pred. No.
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34.2%;
99.8%;
 Query Match 34.2
Best Local Similarity 99.8
Matches 443; Conservative
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ORGANISM: Homo sapiens
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Matches 117; Conser
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GENERAL INFORMATION:
APPLICANT: PANIOWSKI, KZYSZLOF
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1247
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OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HEAR SIGNAL = 3.7
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US-09-864-761-37615
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                             PRIOR APPLICATION UNMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PLING DATE: 2000-01-30
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PRIOR PLING DATE: 2000-01-30
PRIOR PRICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37615
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100.0%; Pred. No. 4.8;
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0.9%; Score 9; UB >
Best Local Similarity 100.0%; Pred. No. 4.8
Matches 9; Conservative 0; Mismatches
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        FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669
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100.0%; Pred. No. 1e-80;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQ 107
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Best Local Similarity 100.(
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-864-761-37615
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24;
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
RECERRENE/POCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
. 10;
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 188, Application US/09438486
; Publication No. US20030009019A1
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, 100.0%; Pred
0, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                             ZIP: 94111
COMPUTER READABLE FORM:
                                            STATE: California COUNTRY: United St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.7
Best Local Similarity 100.
Matches 7; Conservative
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Fatent No. US20020164786A1
GENERAL INFORMATION:
CECH, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Harley, Calvin
TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
NOMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 8; DB 10; Length 446;
100.0%; Pred. No. 17;
Live 0; Mismatches 0; Indels
              RESULT 7

US-09-747-116-2

Sequence 2, Application US/09747116

Patent No. US20010006799A1

GENERAL INFORMATION:
APPLICANT: Wallis, Nicola

TITLE OF INVENTION: NOVEL HISTIDINE KINASE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STRRET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville
STATE: NJ

COUNTY: USA
ZIP: 08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PastSEM: DOS SOFTWARE: PastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/747,116
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,941
FILING DATE:
ATTORNEY: CATTON NUMBER: OB/879,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 446 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
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MEDIUM TYPE: Diskett
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Best Local Similarity
      135 LQEELNQE 142
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220 LQEELNQE 227
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US-09-843-676-188
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Gaps .; 0

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RESULT 11

US-09-864-761-37819

Sequence 37819, Application US/09864761

Sequence 37819, Application US/09864761

Sequence 37819, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-108-03

PRIOR FILING DATE: 2000-10-07

PRIOR FILING DATE: 2000-10-07
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: SATSSPROT HIT: O14607, EVALUE 4.00e-07
OTHER INFORMATION: EST_HUMAN HIT: AA330221.1, EVALUE 7.00e-04
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                            PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/0006/9
PRIOR PLICATION NUMBER: PCT/USO1/0066/9
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PRICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NOS: 49335
LENGTH: 39
            APPLICATION NUMBER: PCT/US01/00667
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP T
OTHER INFORMATION: EXPRE
OTHER INFORMATION: EXPRE
OTHER INFORMATION: EXPRE
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Best Local Similarity
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|17 LKEENEK 23
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APPLICANT: Rank, David R.
APPLICANT: Harzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE OF INVENTION NUMBER: US 60/180, 312
CURRENT FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015389-002931US
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                                                                                                                                                                         PRICE APPLICATION: 309
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06 MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
FILING DATE: 01-CCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
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12-09-864-761-35935
7 Sequence 35935, Application US/09864761
7 Patent No. US20020048763A1
                                                                                              UMBER: US/09/438,486
12-NOV-1999
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0
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-09-438-486-188
                                                                                              APPLICATION NUMBER:
                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       759 TRKPSSG 765
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Gaps
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NN: EXPRESSED IN BT474, SIGNAL = 3.7

NN: EXPRESSED IN BT474, SIGNAL = 3.7

NN: EXPRESSED IN ADDLT LIVER, SIGNAL = 4.4

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN BEAIN, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.7

NN: EXPRESSED IN HELA, SIGNAL = 4.6

NN: EXPRESSED IN HELA, SIGNAL = 3.9

NN: EXT-HUMAN HIT: AW38142.1, EVALUE 5.20e-02

NN: SWISSPROT HIT: P41246, EVALUE 5.00e+00
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                       PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-130
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR PILING DATE: 2001-01-30
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches
US 60/207,456
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP TO AC002470.5
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRE
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Patent No. US200200487631

GRNERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
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N: EXPRESSED IN BT474, SIGNAL = 1.8
N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
N: EXPRESSED IN LUNG, SIGNAL = 1.6
N: EXPRESSED IN LUNG, SIGNAL = 1.6
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN PLACENTA, SIGNAL = 1.9
N: EXPRESSED IN HELAO, SIGNAL = 1.9
N: EXPRESSED IN HELA, SIGNAL = 1.8
N: EXPRESSED IN HELA, SIGNAL = 1.9
N: EXPRESSED IN HELA, SIGN
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100.0%; Pred. No. 18;
Live 0; Mismatches 0; Indels
                       PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
    APPLICATION NUMBER: PCT/US01/00666
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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20 LQPVSPG 26
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US-09-864-761-33346
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US-10-032-159A-10

Sequence 10, Application US/10032159A

Patent No. US20020164703A1

GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100

CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 37

SOFFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 92
                                                                Length 78;
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                                                         Query Match 0.7%; Score 7; DB 10; Best Local Similarity 100.0%; Pred. No. 31; Matches 7; Conservative 0; Mismatches
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US-10-032-159A-10
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24 LTPYLRO 30
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APPLICANT: COLISON, KARI L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramamoto, Robert T.
APPLICANT: Amammoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: IDENTIFYOLES
TITLE OF INVENTION: DATE: 2001-03-21
FRIOR REPERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: GO/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/25,65
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-12-27
FRIOR FILING DATE: 2000-12-27
FRIOR FILING DATE: 2001-02-16
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                                                                          APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENT VET. 1000-08-03
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5287
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US-09-815-242-5046
Sequence 5046, Application US/09815242
; Petent No. US/0000061569A1
; GENERAL INFORMATION:
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ORGANISM: Klebsiella pneumoniae
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17 QEKELAA 23
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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- protein search, using sw model OM protein Run on:

January 22, 2003, 08:56:55 ; Search time 26 Seconds (without alignments) 3712.268 Million cell updates/sec

US-09-767-215-2 1004 Perfect score:

1 MGELCRRDSALTALDEETLW.......VRQAIADEQKKVVWTEQSPR 1004

Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283224 seqs, 96134422 residues Searched:

0

Word size :

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB s Post-processing: Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMADTES

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Score	Query	Length	DB	ID	Description
10		738	7	B69863	two-component sens
œ		162	N	B89894	Ω
80		167	~	н69881	
œ		245	~	XMECNC	~~
80		245	~	A91294	
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σο		270	ď	G71061	hypothetical prote
80		324	~	AB3548	
80		332	~	T26436	$\overline{}$
		346	7	AI2229	Syr
		348	~	T28806	olfactory receptor
		366	7	B75481	•-
	•	381	7	873665	hypothetical prote
	•	388	7	E95177	aminotransferase,
		388	7	G98043	aminotransferase (
		418	7	T45807	translation initia
		446	~	н97929	
		662	7	H95934	probable MPA1 fami
		750	~	T21534	hypothetical prote
		752	٦	S40780	Ψ
		772	~	T27907.	hypothetical prote
		851	7	T06722	-
	٠	996	7	S43878	c
		62	N	T30666	hypothetical prote
		68	~	WZVZA2	7K HindIII-C prote
	•	73	7		hypothetical prote
		74	7	22	hypothetical prote
		9.2	~	9120	hypothetical prote
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0 t -0 t -1.0 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1	Score 10 10 88 88 88 88 88 88 88 77		Action 100 000 000 000 000 000 000 000 000 00	Query Length Langth Length Len	Outer y Match Length DB ID Match Length DB ID 1738 2 B869 167 2 H699 167 2 H6

hypothetical prote hypothetical prote hypothetical prote	hypothetical prote conserved hypothet hypothetical prote alpha, 1-6-glucosi	hypothetical prote hypothetical prote ribosomal protein T-cell receptor al	D5L protein - vari hypothetical prote B6L protein - vari	hypothetical prote galectin-7 - human
B95283 T40431 H84287	T48522 AC3244 T49389 T50029	T30769 T14871 S78145 A31557	E36837 T28442 F72150	AH2322 I55469
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## ALIGNMENTS

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Lebyses two component sensor histidine kinase homolog ykrQ - Bacillus subtilis two-component sensor histidine kinase homolog ykrQ - Bacillus subtilis C; Species: Bacillus S; Broutilet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Brnish, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A; Muthors: Foulgar, D.; Fritz, C.; Fujita, W.; Fujita, V.; Fuma, S.; Galizzi, A.; Galich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino Koetter, P.; Koningstein, G.; Rocha, E.; Rose, S.H.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Stato, T.; Scanl A; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Wannoto, K.; Yata, K.; Yoshida T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tanaka, A.; Tasaton, A.; Tetesten Complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Recession: B69863
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-738 KNUNA, A; Tasatone C; DNA, A; Casatone C; Cher, Control C; Cher, Cher, Control C; Cher, Che

A;Cross-references: GB:299111; GB:AL009126; NID:g2633699; PIDN:CAB13226.1; PID:e11849 A;Experimental source: strain 168 C;Genetics:

A; Gene: ykrQ

Gaps ; 0 Length 738; 0; Indels 1.0%; Score 10; DB 2; 100.0%; Pred. No. 0.35; cive 0; Mismatches Best Local Similarity 100. Matches 10; Conservative Query Match

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# 262 EELNRLKEEN 271 ολ

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hypothetical protein SA1058 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-oct-2001
C;Accession: B89894
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ona, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K. C.; Shibb, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146

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DB 1;
. 15;
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100.0%; Pred. No. 15;
iive 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-14 <MAS>
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|150 GTSEEQLL 157
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Hypothetical protein ylxL.- Bacillus subtilis

NyAlernate names: sign 3'-region hypothetical protein C
C; Species: Bacillus subtilis

NyAlernate names: sign 3'-region hypothetical protein C
C; Species: Bacillus subtilis
C; Species: Bacillus
C; Reco, S; Broutllet, S; Bruschi, C'V; Caldwell, B.; Capuano, V.; Carter, N.M.; Charler, C.; Brustin, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Hemarut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.;
Koetter, P.; Konlngstein, G; Kroph, S.; Knoche, B.; Rose, M.; Levine, A.; Liu, H.; Maadad, S.; Hullo, M.; Heger, M.; Rivoller
V, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivoller
Rieger, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Voshida, R.; Aduthors: Yoshikawa, H.; Zamanoto, H.; Yasmanoto, H.; Yasmanoto, M.; Yasmanoto, M.;
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A; Accession: B89894
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB:BA000018; PID:g13701015; PIDN:BAB42310.1; GSPDB:GN00149
A; Cross-references: strain N315
C; Genetics:
A; Gene
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C;Species: Escherichia coli
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-67 <MAR>
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A; Molecule type: DNA
A; Residues: 1-245 <NMK>
B; Butthand, V; Plunkert III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A; Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from A; Reference number: $56314; MUID:95334362; PMID:7610040
A; Accession: $55688
A; Accession: $55688
A; Accession: $55688
A; Molecule type: DNA
A; Mo
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: C65251
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A;Residues: 1-5,'D',7-245 <BLAT>
A;Cross-references: GB:AE000507; GB:U00096; NID:g2367380; PIDN:AAC77317.1; PID:g17908
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: dnaC
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A; Pathway: DNA biosynthesis
C; Superfamily: DNA replication protein dnaC
C; Keywords: DNA biosynthesis; P-loop
F;106-113/Region: nucleotide-binding motif A (P-loop) #status atypical
F;165-169/Region; nucleotide-binding motif B
C,Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Mar-2002
C;Accession: A28484; S56588; B25124; C65251
R;Nakayama, N.; Bond, M.W.; Miyajima, A.; Kobori, J.; Arai, K.
J. Bond, M.W.; Miyajima, A.; Kobori, J.; Arai, K.
J. Biol. Chem. 262, 10475-10480, 1987
A;Title: Structure of Eschericha coli dnaC. Identification of a cysteine residue pos A;Reference number: A92600; MUID:87280100; PMID:3301836
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Species: Escherichia coli (c. Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002 C. Accession: A91294 A. Hangashon: A91294 A. Hangashon: A91294 A. Hangashon: A91204 A. Hangashon: A. Han
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vegetatible incompatibility protein het-e-1 [imported] - Brucella melitensis (strain C; Species: Brucella melitensis
C; Species: Brucella melitensis
C; Accession: AB3548
C; Accession: AB3548
R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
R; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A; Reference number: AB3552; PMID:117756688
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A; Residues: 1.332 (WIL)
A; Residues: 1.332 (WIL)
A; Cross-references: EMBL:AL110477; NID:e1542121; PIDN:CAB54324.1; CESP:Y113G7B.1
A; Experimental source: clone Y113G7B
C; Genetics:
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: A12229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008918; PIDN:AAL53549.1; PID:g17984458; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bacession: T26436
R;Lennard, N.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20215
A;Reference number: Z20215
A;Reference preliminary; translated from GB/EMBL/DDBJ
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v 100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. 20;
rative 0; Mismatches
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-324 <KUR>
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Best Local Similarity
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283 QKEVLLRR 290
       115 LKEENEKL 122
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T26436
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D86135

Chromosome replication protein DnaC [imported] - Escherichia coli (strain O157:H7, subst Cispecias: Escherichia coli
C; Specias: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C; Accession: D86135
C; Accession: D86136
C; Accession: D86137
C; Accession: D86127
C; Accession: D86
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: A: Pyrococcus horikoshii
C;Species: A: Pyrococcus horikoshii
C;Spate: 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: G71061
R;Kawarabayasi, Y:; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Recession: G71061
A;Recession: G71061
A;Residues: 1-270 cKAW>
A;Rosor-references: GB:AP000005; NID:93236132; PIDN:BAA30289.1; PID:d1031232; PID:932576
A;Rosor-references: GB:AP000005; NID:93236132; PIDN:BAA30289.1; PID:d1031232; PID:932576
A;Roserimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Residues: 1-245 <hAY>
A;Cross-references: GB:BA000007; PIDN:BAB38744.1; PID:g13364799; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS5321
C;Superfamily: DNA replication protein dnaC
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100.0%; Pred. No. 16;
tive 0; Mismatches
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Matches 8; Conservative
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Matches
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RESULT 11

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1381 (41M) A;Residues: 1381 (41M) A;Residues: 1381 (41M) A;Cross-references: EMBL:AE000032; GB:U00089; NID:g1674011; PIDN:AAB95987.1; PID:g167 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Elsen, J.A.; Read, T.D.; Peterson, S.; H on, J.D.; Umayam, L.X.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 496-506, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Ailler: Complete Genome Sequence of a virulent isolate of Streptococcus pneumonlae. A; Accession: E95177
A; Accession: E95177
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-388 < KUR>
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A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73665
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aminotransferase (EC 2.6.1.-) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
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                                                                                                                                                                                                                                                                    hypothetical protein PO2_orf381 - Mycoplasma pneumoniae (strain ATCC 29342) C.Species: Mycoplasma pneumoniae A.Variety: ATCC 29342 A.Variety: ATCC 29342 C.Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999 C.Accession: S73665
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: E95177
                                   Gaps
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Pred. No. 23;
0; Mismatches
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        21;
                                Mismatches
        Pred. No.
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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                                                                                       RVTPGSAA 604
                                                                                                                                        274 RVTPGSAA 281
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|LVSSTESQ 95
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B75481
C;Specias: Delnococcus radiodurans
C;Specias: Delnococcus radiodurans
C;Specias: Delnococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002
C;Accession: B75481
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75481
A;Status: prelliminary
A;Molecule type: DNA
A;Residues: 1-366 <WHID
A;Residues: 1-366 <WHID
A;Residues: 1-366 <WHID
A;Residues: 1-366 <WHID
A;Cross-references: GB:AE001930; GB:AE000513; NID:g6458450; PIDN:AAF10323.1; PID:g645845
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRO745
A;Gene: DRO745
A;Gene: DRO745
A;Gene: DRO745
A;Map position: 1
C;Superfamily: Escherichia coli trypsin-like proteinase; GIGF domain homology; trypsin H
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Offactory receptor ODR-10 - Caenorhabditis elegans
Offactory receptor ODR-10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28806
R;Du, Z.
Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C53B7.
A;Reference number: 220526
A;Accession: T28806
A;Reference number: 220526
A;Accession: T28806
A;Reterence number: 220526
A;Gession: T28806
A;Gession: T28806
A;Genetics: A;Reterences: EMBL:U42830; PIDN:AAC48279.1; GSPDB:GN00028; CESP:odr-10
A;Experimental source: strain Bristol N2; clone C53B7
C;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 65/3; 120/2; 174/2; 196/3; 221/3; 263/3; 323/1
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A;Accession: A12229
A;Status: preliminary
A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-346 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75091.1; PID:g17132487; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: cobw
C;Superfamily: cobw protein
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C: Accession: G98043
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M y. Burn, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Aritle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MuID:21429245; PMID:11544234
A:Accession: G98043
A:Accession: G9
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Search completed: January 22, 2003, 09:00:11 Job time : 30 secs

137 SLVEKDSL 144

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 22, 2003, 08:53:45 ; Search time 16 Seconds (without alignments) 2602.640 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-767-215-2 1004 1 MGELCRRDSALTALDEETLW.....VRQAIADEQKKVVWTEQSPR 1004

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters:

0

Word size :

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			DB		-
			Length	11111	100
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			No. Score Match Length DB ID		1004
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		Description	у	mus mus		bacil		Q9scw4 arabidopsis			P75283 mycoplasma						O21251 reclinomona	_	rhizc		P46103 plasmodium	Q9bw83 homo sapien	-	P74901 thermus the	Q9xt48 macropus eu								P28320 saccharomyc	e.	P19879 bos taurus
SUMMAKIES		ΩI	CARE_HUMAN	CARE_MOUSE	CARB_HUMAN	YLXL_BACSU	DNAC_ECOLI	HSF6_ARATH	PEP1_GADMO	PLSX_CLOTS	YF03_MYCPN	EFGM_RAT	YH07_VACCV	GVPB_BACME	CHLB_PLESC	CHLB_POLCU	RM14_RECAM	LEG7_HUMAN	YN77_RHIME	RPC_BPPH1	DRTS_PLAVN	RAYL_HUMAN	RAYL_MOUSE	VATE_THETH	TNFB_MACEU	RPOC_PROHO	V281_ARATH	V282_ARATH	HIS1_BACHD	RNH_STRCO	JOIN_LYCES	NRTB_SYNY3		BAH_STRHY	OIF_BOVIN
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## ALIGNMENTS

RESULT 1

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AC AC	VB5;
5 5	15-JUN-2002 (Rel. 41, Created)
āā	JUN-2002 (Rel: 41)
DE	pase recruitment domain
DE	
GN	CARD14 OR CARMA2.
SO	
8	Metazoa; Chordata; Craniata; Vertebrata; E
88	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
¥ 2	NCEL_IGXID= 4000;
N C	LT CECTION TO A CECTION OF A CE
RX X	PubMed=11278692:
RA	on M.D., Povet
RA	Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.;
RT	"CARD11 and CARD14 are novel caspase recruitment domain
RT	(CARD)/membrane-associated guanylate kinase (MAGUK) family members
RT	that interact with Bc110 and activate NF-kappaB.";
R.L	J. Blol. Chem. 2/6:118/7-11882(2001).
Z C	[2]
A c	SEQUENCE FROM 10. A.
X a	ed=11356195;
KA	Martinon F., Micheau O., Bonnet D., Thome N
RT	
RI	ø
RL	FEBS Lett. 496:121-127(2001).
N S	[ 3 ]
¥ ;	
KA Pr	Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
2 2	s rect.
Z I	[4]
RP	SEQUENCE OF I-/40 FROM N.A.
) ¥	TISSUE=Cervix, and Colon;
KA 1	J. K. ;
7 K	bmitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
38	FUNCTION: ACCIVE
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ع د	W. Cytopiasmic.
	- Tissue Specificify: Expressed in placenta, Also d
3 8	it not in the other
ع د	SIMILARITY: CONTAINS I
3 5	- SIMILARITI: CONTAINS
ی و	- SIMILARIII: CONTAINS I GUANILAIE NINASE-LINE DOMAIN. - CAMMINN: Supposed to contain a SHO demain which is not
3 5	Supposed to contain a sas Pfam or SMART
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ပ္ပ	European Bioinformatics Institute. There are no restrictions
ပ္ပ	use by non-profit institutions as long as its content is in no

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SEQUENCE OF 82-743 FROM N.A.
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and for commercial
       (See http://www.isb-sib.ch/announce/
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PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
Coiled coil.
                                                                                                                                                       PDZ.
GUANYLATE KINASE.
modified and this statement is not removed.
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        entities requires a license agreement (
or send an email to license@isb-sib.ch)
                             EMBL; AF322642; AAG53403.1; -.
EMBL; AY032927; AAK54453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL; BC001326, AAH01326.1; AIT_INIT.
INTERPRO; IPRO00619; Guanylate_kin.
INTERPRO; IPRO01478; PDZ.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                               840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 GSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bimpl, a MAGUK family member linking protein kinase C activation to Bcl10-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                          YKRLLQDLEAKVATSGDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHR
                                                                                 VNSYTMKDTAAHGTIPNYSRAQQQLIALIQDMTQQCTVTRKPSSGGPQKLVRIVSMDKAK
                                                                                                                                                                                                                                                                                   ASPLRLSFDRGQLDPSRMEGSSTCFWAESCLTLVPYTLVWPHRPARPRPVLLVPRAVGKI
                                                                                                                                                                                                                                                                                                             LSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTH
                                                                                                                                                                                                                                                                                                                                                                                                                            ALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21391892; Pubmed=11387339;
MEDLINE=21391892; Pubmed=11387339;
MEDLINE=21391892; Pubmed=11387339;
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.
Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEGSPR 1004
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PROSITE,
                                                                                                                                                                                                                    Coiled coil.
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P40405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                              Aatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in Hela S3, Molt-4, A549 and G431 cells. Not SIMILARITY: CONTAINS I CARD DOMAIN.
SIMILARITY: CONTAINS I GARD DOMAIN.
SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21255663; PubMed-11356195; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Carmal, a CARD-containing binding partner of Bc110, induces Bc110 phosphorylation and NF-kappa activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;
"CARD11 and CARD14 are novel caspase recruitment domain
(CARD)/membrane-associated guanylate kinase (MAGUK) family members
that interact with Bcll0 and activate NF-kappaB.";
J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylation of Bc110. SUBUNIT: CARD11 and Bc110 bind to each other by CARD-CARD interaction.
                                                                                                                                                   2)
                                                                                                                                                   QAQQQLLA -> HLLEDHRS (IN REF. ; D18350DA12430255 CRC64;
                                                                                                                                                                                 Length 999;
                                                                                                                                                                                                        0; Indels
                                                                                                         CARD.
COILED COIL (POTENTIAL).
                                                               FALSE_NEG.
                                                                                                                                                                                  Score 28; DB 1; Le
Pred. No. 5.9e-20;
                                                                                                                                PDZ.
GUANYLATE KINASE.
                                                                                                                                                                            2.8%; scc.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                        PRT; 1147 AA
                                     Pfam; PF0095; PD2; 1.
PROSITE: PS50209; CARD: 1.
PROSITE: PS0856; GUANTLATE_KINASE_1;
PROSITE: PS50052; GUANTLATE_KINASE_2;
PROSITE: PS50106; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                         80 RGKNGAIAFLESLKFHNPDVYTLVTGLQ 107
          EMBL; BC004692; AAH04692.1; -.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-21192234; PubMed-11278692;
                                                                                                                                                             113496 MW;
EMBL; AF363457; AAK60137.1; -.
                                                                                                                                                                                                       28; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                   411
655
986
743
                                                                                                         15
125
572
854
736
799 AA;
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        3) (Carma 1).
CARD11 OR CARMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                              Coiled coil.
DOMAIN
                                                                                                                                                                                                                                                                                                       CARB_HUMAN
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                 Query Match
                                                                                                                                                   CONFLICT
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                                                                                                                    DOMAIN
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Bruschic V., Brans A., Braun M., Bitjanell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Parro V., Pohl T.M., Portetelle B., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Supposed to contain a SH3 domain which is not detected by Pfam or {\tt SMART}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLATE KINASE.
P -> L (IN REF. 2).
W: 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL). PDZ.
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FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 1;
Pred. No. 2.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00228; PDZ; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANUATE_KINASE_1;
PROSITE; PS50052; GUANVLATE_KINASE_2;
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein ylxL precursor
                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808
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123
673
77
966
111
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811
808
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764 TSGDSFYIR 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis
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Biol. Chem. 263:15083-15093(1988).
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Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takhashi H., Takemaru K., Tarekeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Weller H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yasumoto K., Yatu K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              Helmann J.D., Marquez L.M., Chamberlin M.J.;
"Cloning, sequencing, and disruption of the Bacillus subtilis sigma
28 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakayama N., Bond M.W., Miyajima A., Kobori J., Arai K.-I.; Structure of Escherichia coli dnaC. Identification of a cysteine residue possibly involved in association with dnaB protein."; J. Biol. Chem. 262:10475-10480(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masai H., Arai K.-I.; "Operon structure of dnaT and dnaC genes essential for normal and stable DNA replication of Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 8; DB 1; Length 167;
100.0%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROTEIN YLXL. 356021A73B679B69 CRC64;
                                                                                                                                                                                                                                                                                                                                                              EMBL; M20144; ....-
Subtilist; BG10752; ylxL.
Hypothetical protein; Signal; Complete proteome.
19 POTENTIAL.
19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-A0G-1988 (Rel. 08, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
DAA replication protein dnaC.
DNAC OR DNAD OR B4361 OR Z5961 OR ECS5321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                       Bacteriol. 170:1568-1574(1988).
                                                                                                                                                       SEQUENCE OF 1-67 FROM N.A. MEDLINE-88169477; Pubmed-2832368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIKAIN=A12;
MEDLINE=87280100; PubMed=3301836;
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                                                                                                                                                                                                                                                                                                                                                                                                                            167 AA; 19119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                  EMBL; 299112; CAB13521.1;
                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia.
NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 LKEENEKL 274
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P07905;
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Matches
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"Cloning of the Escherichia coli gene for primosomal protein i: the relationship to dnar, essential for chromosomal DNA replication.";
Proc. Natl. Acad. Sci. U.S.A. 83:1256-1266(1986).
-!- FUNCTION: THIS PROTEIN IS REQUIRED FOR CHROMOSOMAL REPLICATION. IT FORMS, IN CONCERT WITH DNAB PROTEIN AND OTHER PREPRIMING PROTEINS DNAT, N, N' N' N' A PREPRIMING PROTEIN COMPLEX ON THE SPECIFIC SITE OF THE TEMPLATE DNA RECOGNIZED BY PROTEIN N'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterchemorrhagic Escherichia coli O15:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLY INVOLVED IN THE INTERACTION WITH THE DNAB PROPEIN.

D -> A (IN REF. I AND 6).

CSCC7232221FIIFI CRC64;
                                                                                                                                                                                    "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                              Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA replication; Primosome; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86149284; PubMed-3006041;
SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed=7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECO2DBASE; 1030.3; 6TH EDITION. ECOGene; EG10237; dnaC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000507; AAC77317.1; -. EMBL; AE005667; AAG59544.1; -. EMBL; AP002569; BAB38744.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J04030; AAA23700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U14003; AAA97260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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PIR; B25124; B25124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                     Blattner F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B2512,
ECO2DBASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Length 245;

DB 1;

Score 8;

0.8%;

us-09-767-215-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Columbia; TISSUE=Green siliques;
Schoefil F., Praendl R.;
"De-repression of heat shock protein synthesis in transgenic plants.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat shock factor protein 6 (HSF 6) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-cv. Columbia;
MEDLINE-99087489; PubMed-9872454;
Makamura Y., Sato S., Asamizu E., Kaneko I., Kotani H., Miyajima
Tabata S.;
                                                 ö
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HÖMOTRIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (By similarity).
PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04D86398693B1997 CRC64;
                                                 0;
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                         Pred. No. 5.9;
                                                                                                                                                                                                                                                                           299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
POLY-ASN.
POLY-GLU.
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: AB016880; BAB10163.1; -.
HSSP; P22813; 1HKT.
InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR00341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00056; HSFDOMAIN.
ProDom; PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF; 1.
100.0%; Pic
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                                                                                                                                                                                                                                                                                                                                                                                                                             6) (HSTF 6).
HSF6 OR AT5G62020 OR MTG10.4.
                                                 8; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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                         Best Local Similarity
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                                                                                                943 GTSEEQLL 950
                                                                                                                               150 GTSEEQLL 157
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SEQUENCE
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HSF6_ARATH
                                              Matches
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"Structure and proposed amino-acid sequence of a pepsin from Atlantic
cod (Gadus morhua).";
                                    Gaps
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                                                                                                                                                                                                                                                                                                                 Gadus morhua (Atlantic cod).

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:
Acanthomorpha: Paracanthopterygii: Gadiformes: Gadidae: Gadus.
NCBI_TaxID=8049;
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van Rinsum A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN FATTY ACTO OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acta Crystallogr. D 5.32-46(1998).

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.

PDB: JAME; 24-DEC-97.

InterPro: IPR001461; Aspprotease_1:

InterPro: IPR001369; Aspprotease_site.

InterPro: IPR001969; Aspprotease_site.

PRIMITS: PR00792: PEPSIN.

PROSITE: PS00141; ASP_PROTEASE; 2.

PRINTS: PR00792: PEPSIN.

PROSITE: PS00141; ASP_PROTEASE; 2.

PROSITE: 214 214 BY SIMILARITY.

ACT_SITE 214 214 BY SIMILARITY.

DISULFID 206 209 BY SIMILARITY.

DISULFID 206 209 BY SIMILARITY.

DISULFID 206 324 AA; 34014 MW; EE3A6097B6941DD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thermosaccharolyticum).
Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
Length 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fatty acid/phospholipid synthesis protein plsX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacteriaceae; Thermoanaerobacterium
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DB 1;
                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1992 (Rel. 41, Last annotation update)
Pepsin IIB (EC 3.4.23..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AA.
                                                                                                                                                                                                       324 AA
                 Pred. No. 7;
Mismatches
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Mismatches
0.8%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                       PRT;
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100.0%; PI
0.0°,
100.08; Piv
                                    8; Conservative
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nes 8; Conser
                 Best Local Similarity
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                                                                       269 EENEKLRS 276
                                                                                            177 EENEKLRS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 SQSLVEKD 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Stomach;
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O65984;
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Query Match
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                                  Matches
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Conservative
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                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                 NCBI_TaxID=10116;
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P17357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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NP_BIND
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                  QQ
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B -C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 8; DB 1; Length 381;
100.0%; Pred. No. 8.8;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             Length 333;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very hypothetical mgpC-like protein MPN503 (P02_orf381).
MPN503 OR MP339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein; Complete proteome.
381 AA; 40896 MW; 5CFD05505E344852 CRC64;
                                                                                                                                                                                                                                                             Fatty acid biosynthesis; Phospholipid biosynthesis.
SEQUENCE 333 AA; 35930 MW; 8A932B1A96D88EC9 CRC64;
                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                   0.8%; Scor.
100.0%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE MGPC FAMILY.
PHOSPHOLIPID SYNTHESIS (BY SIMILARITY). SIMILARITY: BELONGS TO THE PLSX FAMILY.
                                                                                                                                                                                 EMBL; AJ004870; CAA06178.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                              InterPro IPR003664; FA_synthesis.
Plan; FP02504; FA_synthesis; 1.
ProDom; PD006674; FA_synthesis; 1.
TIGRPAMS; TIGR00182; plsX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129; '
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000032; AAB95987.1; -.
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               1111111
241 LLKQELQR 248
                                                                                                                                                                                                                                                                                                                                                                              228 LLKQELQR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 LVSSTESQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Mitochondrial.
-!- TISSUB SPECIFICITY: DETECTED IN ALL TISSUES WITH THE HIGHEST LEVEL IN LIVER, THYMOS AND BRAIN.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                       factor G in mammals.";
Nucleic Acids Res. 21:2641-2647(1993)
-!- FUNCTION: THE PROPEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-93324327; PubMed-8332461; Barker C.S., Makris A., Patriotis C., Bear S.E., Tsichlis P.N.; "Identification of the gene encoding the mitochondrial elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELONGATION FACTOR G.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fram; PF00679; EFC_C; 1.

Pfam; PF03144; GTP_EFTU_D2; 1.

TIGRFAMS; TIGR00231; small_GTP; 1.

TIGRFAMS; TIGR0048; EF-G; 1.

PROSTIE; P500301; EFACTOR_GTP; 1.

Transit peptide; GTP_binding.
                                                01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor G, mitochondrial precursor (MEF-G).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 15, Created)
(Rel. 15, Last sequence update)
752 AA.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000640; EFG_C.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR00055; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF00679; EFG_C; 1.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.88;
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InterPro; IPR004540; EF-G.
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01-AUG-1990 (
01-AUG-1990 (
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ID YH07_V
AC P17357
DT 01-AUG
DT 01-AUG
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InterPro; IPR000638; Gas_vesicle.
                                                                                                        Query Match
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Matches
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    DR DR DR SQ SQ
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression in Escherichia coll.";
J. Bacteriol. 180:2450-2458(1998).
-!- FUNCTION: Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth. GvpA type proteins form the essential core of the structure.
-!- SUBCELLULAR LOCATION: GAS VESICLE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE A FAMILY.
                                                                                                      MEDLINE-89073756; PubMed-2849238;
Kotwal G.J., Moss B.;
"Analysis of a large cluster of nonessential genes deleted from
vaccinia virus terminal transposition mutant.";
Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Fĭrmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                         Length 68;
                                                                                                                                                                                                                                                                                                    PIR; B31829; WZVZA2.
Hypothetical protein; Early protein.
SEQUENCE 68 AA; 7814 MW; 47DF7558D134D949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gas vesicle structural protein B (GVP B).
01-FEB-1991 (Rel. 17, Last annotation update)
Hypothetical 7.8 kDa HINDIII-C protein.
                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                 0.7%; Sco.
100.0%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VT1660;
MEDLINE=98233742; PubMed=9573198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF053765; AAC38416.1; -.
                                                                                                                                                                                                                                                                                         EMBL; M22812; AAA69593.1; -.
                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.vv
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                         SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                            702 VLHVTDT 708
                                                                                                                                                                                                                                                                                                                                                                                                                           111111
36 VLHVTDT 42
                                                      Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (
15-JUN-2002 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPB_BACME
068677;
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GVPB_BACME
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A Boivin R., Richard M., Beauseigle D., Bousquet J., Bellemare G.:
Boivin R., Richard M., Beauseigle D., Bousquet J., Bellemare G.:
"Phylogenetic inferences from chloroplast chilb gene sequences of
"Phylogenetic inferences from chloroplast and diverse land plants."

T methrolepis exaltata (Filicopsida), Ephedra altissima (Gnetopsida),
and diverse land plants."

Definition of the phylogenet. Evol. 6:19-29(1996).

T mol. Phylogenet. Evol. 6:19-29(1996).

Protochlorophyllide (Pchlide) to form chlorophyllide a (Chlide)

(By similarity). This reaction is light-independent.

-!- PATHWAY: Light-independent chlorophyll biosynthesis.

-!- PATHWAY: Light-independent chlorophyll biosynthesis.

-!- SUBUNIT: Protochlorophyllide reductase is thought to be composed of three subunits; chll., chlN and chlB. Could form a heteroteetramer of two chlB and two chlN subunits (By similarity).

C -!- SIMILARITY: BELONGS TO THE CHLB / BCHB / BCHZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Photosynthesis; Chlorophyll biosynthesis; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Bryidae; Hypnales; Hylocomiaceae; Pleurozium.
NCBL_TaxID=34163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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01-CCT-1994 (Rel. 30, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Light-independent protocollorophyllide reductase subunit B
(EC 1.18.-.) (LI-POR subunit B) (PPOR subunit B) (Fragment).
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100.0%; Pred. No. 27;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA; 11659 MW; 40B101BE6D66B5E0 CRC64;
                                                                                                                                                                           5F089DE77358D84A CRC64;
                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AA
                                                                                                                                                                                                                                       0.7%; Score 7; DB 1
100.0%; Pred. No. 24;
iive 0; Mismatches
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Pfam; PF00148; oxidored_nitro; 1.
Pfam; PF00741; Gas.vesicle; 1.
Probom; PD003598; Gas.vesicle; 1.
PROSITE; PS00234; GAS.VESICLE.A.1; 1.
PROSITE; PS00669; GAS.VESICLE.A.2; 1.
                                                                                                                                                                           9618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pleurozium schreberi (Moss).
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                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
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                                                                                                                                                                           88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               59 EAVGLLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||||
1 KRLLQDL 7
                                                                                                                                               Gas vesicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLB_PLESC
P37854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
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SEQUENCE
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8

STRAIN-ATCC 50394;

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Pfam; PF00148; oxidored_nitro; 1.
Oxidoreductase; Photosynthesis; Chlorophyll biosynthesis; Chloroplast.
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                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Polytrichopsida; Polytrichales; Polytrichaceae; Polytrichum.
NCBI_TaxID=3213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Light-independent protochlorophyllide reductase subunit B
(EC 1.18.-.-) (LI-POR subunit B) (Pragment).
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100.0%; Pred. No. 27;
Live 0; Mismatches 0; Indels
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100 AA: 11573 MW; 984F131F432400A3 CRC64;
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RPL14.
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update
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NCBI_TaxID=48483;
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                                                                                                                                                                                                                                                                                                                                                                                Polytrichum commune (Moss).
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Matches 7; Conservative
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                                                                                                 STANDARD;
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15-DEC-1998
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021251;
                                                                                             CHLB_POLCU
P37852;
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SEQUENCE
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RM14_RECAM
                                RESULT 14
CHLB_POLCU
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MEDLINE-97311393; PubMed-9168110;
Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
Lemieux C., Sankoff D., Turmel M., Gray M.W.;
"An ancestral mitochondrial DNA resembling a eubacterial genome in
                                                                                                                                               Nature 387.497.497(1997).
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE L14P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13415 MW; F942C64410D4EE53 CRC64;
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100.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Job time : 20 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00238; Ribosomal_L14; 1. ProDom; PD001093; Ribosomal_L14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO1067; rplN bact, 1.
PROSITE; PS00049; RIBOSOMAL_L14; 1.
Ribosomal protein; Mitochondrion.
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InterPro; IPR000218; Ribosomal_LL14.
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Matches 7; Conservative
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                                                                                                                            miniature.
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Q9zseO pinus radia Q8yd7O brucella me Q9u2yl caenorhabdi Q18807 caenorhabdi

OByrg2 anabaena sp O9rwc4 deinococcus O97ps5 streptococc

Q9h6g7 homo sapien Q9m218 arabidopsis Q60552 mesocricetu

Q8XQ66 neurospora Q9m4t7 arabidopsis Q9C23 arabidopsis Q9C253 erreptococc Q8rsb5 halomonas c Q9bkq7 caenorhabdi Q43060 porphyridiu Q43061 porphyridiu Q9fhk7 arabidopsis Q92vg1 rhizobium m Q8xvg1 ralstonia s Q8xvg1 ralstonia s Q8xvg1 caenorhabdi

Q924i0 mus musculu Q921d6 mus musculu Q23529 caenorhabdi O15083 homo sapien Q9acu8 streptomyce

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

Database :

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SEQUENCE FROM N.A.
Witthuhn V.C. Jr., Donohue T.J.;
Sidhithely regulates transcription of Rhodobacter sphaeroides
gene products involved in formaldehyde oxidation.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR435819; AAL30776.1;
SEQUENCE 390 AA; 41929 MW; BDA7AC33D3F5AE84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 2; Length 390;
Pred. No. 0.33;
0; Mismatches 0; Indels
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09RRC4
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09H667
09M218
08X086
09M4T7
09C523
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09F8K7
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Q18807
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
YKRQ protein.
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nes 10; Conservative
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NCBI_TaxID=1063;
01-MAR-2002
01-MAR-2002
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Query Match
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Q99ug3 staphylococ
Q9an71 bradyrhizob
Q9fsr5 oryza sativ
O58907 pyrococcus
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Q9hcq3 homo sapien
Q9hcq3 homo sapien
Q9su22 drosophila
P91635 drosophila
Q8wu84 homo sapien
Q9tes3 homo sapien
Q9tes4 homo sapien
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Q9nft4 trichomonas
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4309.819 Million cell updates/sec
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                                                                                   ; Search time 48 Seconds
          5.1.3
Compugen Ltd.
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                                                                                                                                                                                                                          671580 segs, 206047115 residues
          GenCore version
Copyright (c) 1993 - 2003
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                                                          protein search, using sw model
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6 031661
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08WUB4
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Q9AN71
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Gapop 60.0 , Gapext 60.0
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sp_human:*
sp_invertebrate:*
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sp_rodent:*
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sp_phage:*
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sp_bacteria:*
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sp_mhc:*
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Result

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RESULT 3
                  Q9NFT4
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Boustaer L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connetron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollghtly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Mostetter P., Koningstein G., Kroph S., Kumano M.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott R.,
RA Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeber, Rose M., Sato T.,
RA Takeuchi M., Tamakoshi A., Takagi T., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Takagi T., Takemaru R.,
RA Voshida K., Wanbutt R., Wedler H., Weitzeneyger T.,
RA Winters P., Wimpat A., Tamamoto H., Yamane K., Yasamoto K., Yasamoto K., Yasamoto K., Yasamoto K., Yasamoto E., Phills P., Phills P., Phills R., Phills P., Phills R., Rose M., Danchin A.;
R. Toshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
R. Toshila F., Phills R., Rose M., Poshikawa H., Danchin R.,
R. Toshila K., Poshikawa H.F., Zumstein E., Poshikawa H., Danchin R.,
R. Toshila F., Poshikawa H.F., Zumstein E., Poshikawa H., Danchin R.,
R. Toshi R., Poshikawa H.F., Zumstein E., Poshikawa H.S., Danc
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
C. -i - SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
EMBL; 299111; CAB13256.1; --
InterPro; IPR003594; ATPbind_ATPase.
R InterPro; IPR004358; Bact_sens_pr_C.
R InterPro; IPR004358; Bact_sens_pr_C.
R InterPro; IPR004359; HIS_KIN_sig.
R InterPro; IPR004359; HIS_KIN_sig.
R InterPro; IPR0014; PAS_domain.
R Pfam; PF00518; PAS; 3.
R Pfam; PF00512; signal; 1.
R Pfam; PF00512; signal; 1.
R PRINTS; PR00344; BCTRLSENSOR.
R SMART; SM00381; Hiska; 1.
R SMART; SM00381; Hiska; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                              Bacteria: Firmicutes: Bacillus/Clostridium group: Bacillales;
Bacillaceae: Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00091; PAS; 4.
TIGRFAMs; TIGR00229; sensory_box; 4.
Kinase; Phosphorylation; Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 10; DB 16; Length 738; 100.0%; Pred. No. 0.58; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738 AA; 85513 MW; FE27DAB7F08AC64B CRC64;
                                                                                                                                    STRAIN-168;
MEDLINE-98044033; PubMed-938437<u>7</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                  SEQUENCE FROM N.A.
                    Bacillus subtilis.
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SEQUENCE 738 AA
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Sano R., Juarez C., Ito M., Banks J.A., Hasebe M.; "KNOX class of homeobox genes potentially have similar function in both sporophytic unicellular and multicellular meristems, but not in gametophytic meristems."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.
NCBL_TaxID=49495;
                                                                                                                                                                                                                                             MEDLINE=20382201; PubMed=10928457;
Bricheux G., Coffe G., Bayle D., Brugerolle G.;
Bricheux G., Coffe G., Bayle D., Brugerolle G.;
"Characterization, cloning and immunolocalization of a coronin homologue in Trichomonas vaginalis.";
Eur. J. Cell Biol. 79:413-422(2000).
-!- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AJ271374; CAB76208.1;
-. InterPro; IPR001680; WD40.
Prodom: PP00400; WD40.
Prodom: PP0040018; WD40.
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                                                                                                                                                        Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB043954; BAB18582.1; -.
HSSP; P41778; 1DU6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50082; WP_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 435 AA; 48204 MW; F63ADC16D5DCE6C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3EBFCE074AAE080B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 9; DB 10; 100.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9; DB 5;
Pred. No. 4.1;
435 AA.
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PROSITE: PS50071; HOMEDBOX_2; 1.
SEQUENCE 512 AA; 57195 MW; 3EBFCE074P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=HNN; TISSUE=SHOOT APEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000010; Homeobox; 1. SMART; SM0389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.98;
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PRELIMINARY;
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                                                                                                                                     Trichomonas vaginalis.
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) (PI3-kinase) (PtdIns-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase).
PI3K59F OR PI3K-59F OR CG5373.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                Gaps
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WIEDLINE-97184674; PubMed=9032475;
Linassier C., MacDougall L.K., Domin J., Waterfield M.D.;
Linassier C., MacDougall L.K., Domin J., Waterfield M.D.;
"Molecular cloning and biochemical characterization of a Drosophila
phosphatidylinositcl-specific phosphoinositide 3-kinase.";
Fight CATALYTYT ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
EMBL; X99912; CAA68185.1; -
FIJBASE; FREGNO015277; PI3K59F.
InterPro; IPR001263; PI3K-C2.
InterPro; IPR001263; PI3K-C2.
InterPro; IPR001420; PI3R-C2.
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01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
Hypothetical 113.9 kDa protein (Fragment).
Homo sapiens (Human).
Bukaryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      Length 949
                                                                Indels
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8.2;
   0.9%; Score 9; DB 5;
100.0%; Pred. No. 8.2;
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                           100.0%; Pred. No. 8.2
live 0; Mismatches
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Pfam; PF00792; P13KC2; 1.
Pfam; PF0045; P13KC2; 1.
SMART; SM00145; P13Ra; 1.
SMART; SM00146; P13Ra; 1.
PROSITE; PS00916; P13_4_KINASE_2; 1.
PROSITE; PS00916; P13_4_KINASE_2; 1.
PROSITE; PS009096; P13_4_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                             9; Conservative
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=OREGON R;
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tes 9; Conserv
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                                                                                                                                                        443 LSDLSATSS
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SEQUENCE
      Query Match
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P91635
ID P91635
AC P91635
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Chapteron M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Liao G., Miranda A., Mungail C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Xu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AYOS332: AAL13591.].
RES. PRO015277: P13K59F.
RICEPTO: IPRO01263; P13Ka.
InterPro: IPRO01263; P13Ka.
InterPro: IPRO04043; P13L4_Kinase.
Rem: PF00413; P13Ka.
InterPro: PF00413; P13Ka.
InterPro: PF00415; P13L4_Kinase.
Rem: PF00454; P13_P14_kinase; 1.
Rem: PF00454; P13_P14_kinase; 1.
Rem: PF00454; P13_P14_kinase; 1.
Rem: PF00454; P13_P14_kinase; 1.
Res. PROSITE; PS00916; P13_4_KINASE_1; UNKNOWN.].
ROSITE; PS00916; P13_4_KINASE_2; UNKNOWN.].
ROSITE; PS00916; P13_4_KINASE_2; UNKNOWN.].
ROSITE; PS00916; P13_4_KINASE_3; 1.
ROSITE; PS00916; P13_4_KINASE_3; 1.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Sperm antigen.
HCMOCT-1.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HCMMOGT-1.";
"HCMOGT-1.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB041533; BAB16440.1; -.
SEQUENCE 759 AA; 84920 MW; A88E5853B3E4269A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
0;
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                                                                                                                                                                                                                                                                759 AA
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   Mismatches
                                                                                                                                                                                                                                                                   PRT;
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0
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   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                          SFRSSSPAP 478
                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 RLKEENEKL 274
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PI3K59F OR CG5373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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001-D
DT 01-D
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09HCQ3
1D 09HCQ4
AC 09HCQ6
DT 01-M2
DT 01-M3
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ID Q9H6O4
AC Q9H6O4;
DT 01-MAR-20
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
P13K59F protein.
P13K59F or CG5373.
Drosophila melanogaster (Fruit fly).
Brkaryota; Merazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Merazoa, Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                              Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC021123; AAH21123.1;
InterPro; IRR001715; Calponin-like.
Pfam: PF00307; CH: 1.
SMART: SM00033; CH: 1.
Hypothetical protein.
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8.8;
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100.0%; Pred. No. c
0; Mismatches
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MEDLINE-20196006; Pubmed=10731132;
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Matches 9; Conservative
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  SEQUENCE FROM N.A.
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Smith H.O.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhen Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smit Gibbs R.A., Whers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

E Science 287:2185-2195(2000).

"R EMBL; AR604361; AAF47030.1; -.

"Interpro; IPR001577; P35859F.

Interpro; IPR001577; P563V.kin.

"Interpro; IPR001211; PhospholipaseA2.

"Interpro; IPR001213; P183K.C2.

"Interpro; IPR000403; P134K.21.

"R Ffam; PF000613; P134K.21.

"R Ffam; PF000613; P134K.21.

"R Ffam; PF000454; P132-P14_Kinase.

"R FMART; SM00145; P134K.21.

"R SMART; SM00145; P134K.21.

"R PROSITE; PS000445; PGCY_KINASES_2; UNKNOWN_1.

"R PROSITE; PS00015; P134_KINASE_2; UNKNOWN_1.

"R PROSITE; PS00016; P13-4_KINASE_2; UNKNOWN_1.

"R PROSITE; PS00016; P13-4_KINASE_2; UNKNOWN_1.

"R PROSITE; PS00016; P13-4_KINASE_2; ...

"R PROSITE; PS00016; P13-4_KINASE_3; ...

"R PROSITE; PS00016; P13-4_KINASE_3; ...

"R PROSITE; PS00016; P13-4_KINASE_3; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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100.0%; Pred. No. 9.9;
iive 0; Mismatches
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Best Local Similarity
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nes 9; Conserv
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Lancet 357:1225-1240(2001).
                                                                                                                         NCBI_TaxID=158878, 158879;
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                                                                                        Staphylococcus aureus
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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29 KRLLQDLE 36
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                                                                                                                  Staphylococcus
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SEQUENCE FROM N.A.

CSTAIN-CZA / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed-11932384;

A aladan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A ritzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A llen N., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Limmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Gluss A.M.,

Hedderich R., Ingaram-Gmith C., Ruettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Retry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulisen I.,

Metcalf W.W., Birren B.;

A Metcalf W.W., Liu W. Swanson R.V., Zinder S.H., Lander E.,
                                                                                                               Okamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
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                                                                                 SEQUENCE FROM N.A.

TISSUB-SMALL INTESTINE;

Awabate A., Hikili T., Kobatake N., Inagaki H., Ikema Y., Okamoto Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T. Tanaka T., Nakamura Y., Isogai T., Sugano S.;

Tanaka T., Nakamura Y., Isogai T., Sugano S.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO26370; BAB15463.1;

SEQUENCE 143 AA; 15296 MW; CICBCF31219EBDF9 CRC64;
            Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22717 fis, clone HSI13737.
                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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100.0%; Pred. No. 17;
Live 0; Mismatches
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Pred. No.
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EMBL: AEO11170; AAM07840.1; -.
COmplete proteome.
SEQUENCE 157 AA; 18084 MW:
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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106 EEAVGLLR 113
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                                                                                                                                                                                                                                                                            11 SSPAPPSQ 18
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                                                                                                                                                                                                                                                                                                                                                                Q8THL4;
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BENBL: AF322013; AA660905-11; SEQUENCE 223 AA; 25398 MW; 6F86C3C1D5D70315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R. I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
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Bradyrhizobium group; Bradyrhizobium.
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0
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypochetical protein SAV1215.
SAV1215 OR SAL058.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
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EMBL; AP003135; BAB42310.1; -.
InterPro; IPR000181; Pep_deformylase.
Pfam; PF01327; Pep_deformylase; 1.
PRINTS; PR01576; PDEFORMYLASE.
ProDom; PD003844; Pep_deformylase; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 162 AA; 18102 MW; 8E22824A4B2945AF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 25;
ative 0; Mismatches
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100.0%; Pred. No. 19;
tive 0; Mismatches
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the Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
A Tang Y.S., Zhao Q., Liu Y.L., Wu J., Yu Z., Fan D.L., Chen L.,
Weng Q.J., Zhang Q., Lu Y.Q., Yu S.L., Zhu J., Liu X.H. Hu X.,
Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
Hu H.Y., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
A Hu H.Y., Li T., Qian Y.M., Ying K., Hong G.F.;
The Clore: HO212B02.";
The Clore: HO212B02.";
The Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL42007; CAC09359.1;
TherPro; PR001036; Homeobox.
ProDom; PD000010; Homeobox.
PROSITE; PS50071; HOMEOBOX. 1.

PROSITE; PS50071; HOMEOBOX. 2; 1.
PROSITE; PS50071; HOMEOBOX. Nuclear protein.
SEQUENCE 262 AA: 29004 MW; C54C573691F8CBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                 Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 16, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (Archae)
01-MAR-2016
01-MAR-2016
01-MAR-2019
01-MAR
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Q9FSR5;
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473 SSSPAPPS 480

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January 22, 2003, 08:49:35; Search time 20.8535 Seconds (without alignments) 683.714 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	Description	! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !	AAE07165 Human predicted ca			AAU73247 Human plakoglobin					
S	ΙD		AAE0	AAU0	AAU0	AAU7	AAU0	AAB4	ABP1	AAB9	AAIIO
	DB	22	22	22	22	23	22	21	23	22	22
	Query e Match Length DB 1	1004	1139	1147	1032	1032	536	174	174	366	536
đ	Query Match	100.0	100.0	48.2	43.9	43.9	38.8	37.3	37.3	37.3	37.3
	Score	560	260	270	246	246	217	209	209	209	209
	Result No.	1	7	m	4	5	9	7	∞	σ	10

Human CIPER protei Mouse CIPER protei Drosophila melanog CTA1-OVA-DD fusion Human Voltagae-gate Human polypeptide, Human polypeptide, Human Voltagae-gate Human Voltagae-gate Human Voltagae-gate Human Voltagae-gate Human Voltagae-gate Human OSEPSOBIII amelanog Hemolysin. Serpul Human ORFX ORF2683 Mouse LICAM FN4-5 MOUSE LICAM FN4-5 MOUSE LICAM FN3-5 MOUSE LICAM FN3-5 MOUSE LICAM FN4-5 MOUSE LICAM FN3-5 MOU	4 (CARD-14).  4 (CARD-14).  14; CARD-14; chromosome 17;  1 growth; cell death; cancer; therapy;  1 growth; cell death; cancer; therapy;  2 erythematosus; neurological disorder;  1 lasease; inflammancry disorder; anaemia;  1 lasease; allergic rhinitis; infection;  1 isease; allergic rhinitis; infection;  1 c; immunosuppressive; nootropic;  1 ccferial.  1 cGMP-dependent protein kinase  2 cGMP-dependent protein kinase  3 cGMP-dependent protein site"  ase II phosphorylation site"  ase II phosphorylation site"
AAU73245 AAX59413 ABB62651 AAB52413 AAB22544 AAX44570 AAM93314 AAX44551 AAM93314 AAX44571 AAX44572 AAM93214 AAX44572 AAM93214 AAX4572 AAG90700 ABB60521 AAX44572 AAG90700 ABB60521 AAX46573 AAY10658 AAV10656 AAU10656 AAU10668 AAU10669 AAU10670 AABB77378 AAN70608 AAU10669 AAU10669 AAU10669 AAU10670 AABB77378 AAU10669 AAU10669 AAU10670 AABB77378 AAU10669 AAU10669 AAU10670 AABB77378 AAU10669 AAU10670 AABB77378 AAU10669	14 A Minion-11 Indo Coel Coel Coel Coel Coel Coel Coel Coe
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/note= "N-glycosylation site"
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                                                                                           'note= "N-myristoy<sub>1atto...</sub>
121.123
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e= "Casein kinase II phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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-- "Protein Kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site"
                                                                                                                                                                                                                                          ...168
ce= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                     ..243
.e- "Casein kinase II phosphorylation site"
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                                       "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365
ce= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                     .227
e= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .381
e= "Casein Kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                        .256
e= "Casein Kinase II phosphorylation
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e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .406
e= "Leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587..592
/note= "N-myristoylation site"
589..592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .516
e= "N-myristoylation site"
                                                                                                                                                             . 135
te= "N-myristoylation site"
                                                                                                                                                                                                                               "N-myristoylation site"
                                                                              .122
e= "N-myristoylation site"
                                                                   "N-glycosylation site"
                                                                                                                                                  label= Coiled_Coil_domain
                                                                                                                                                                                                                                                                                                                                         label= k-Box_domain
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60. 763
// Anote= "CAMP- and CGMP-dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                 85._793
/note= "Peroxisomal targetting signal"
796..799
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                      rocte= "Protein Kiuuss . . .
725..728
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                   note= "N-glycosytuctor".
159..761
/note= "Protein kinase C phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
                               "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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"Casein kinase II phosphorylation site"
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193..896
Anote= "Casein kinase II phosphorylation"
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e= "Casein kinase II phosphorylation
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.e= "Protein kinase C phosphorylation
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te= "Casein kinase II phosphorylation
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ce= "Peroxisomal targetting signal"
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== "RGD cell attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Guanylate_kinase_domain
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100..805
/~~+e= "N-myristoylation site"
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1002..1004
                                                                                                                                         .719
e= "N-myristoylation site"
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e= "N-glycosylation site"
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RESULT 3
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                                                       The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and ParkInson's disease, inflammatory disorders, haematological disorders (e.g., anaemia myelodysplastic syndromas), myocardial infarctions, strokes, immune disorders (e.g., corbn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                         10 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
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                                                                                                                                                                                                                                            ; DB 22;
1.6e-64;
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100.0%; Pred. No. 1.6
:ive 0; Mismatches
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700
                                   Claim 1; Fig 1A-1E; 109pp; English.
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Matches 107; Conservative
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                                                                                                                                                                                                                    1004 AA;
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An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ALTALDEETLWEWMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; caspase recruitment domain; CARD-11; Bc1-10; NF-kappaB;
apoptosis; hyperproliferative disorder; autoimmune; neurological;
inflammatory disorder; viral infection; stress-related response.
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168..171
176.e= "Casein kinase II phosphorylation site"
175..183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 560; DB 22; 100.0%; Pred. No. 1.9e-64;
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                                                                                                               Disclosure; Fig 2A-2C; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU01207;
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/note="N-glycosylation site"
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e= "Casein kinase II phosphorylation site"
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re- "Protein Kinase C phosphorylation site"
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ce= "Casein kinase II phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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.e- "Casein kinase II phosphorylation site"
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:e- "Protein kinase C phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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tem "Casein kinase II phosphorylation site"
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 'note= "Tyrosine kinase phosphorylation site"
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te= "Casein kinase II phosphorylation
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e- "Tyrosine kinase phosphorylation
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.e= "N-myristoylation site"
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te= "N-myristoylation site"
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/note= "N-glycosylation site"
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The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell DDNA library. Also described are coverabled are according to the sequences for CARD-9 and CARD-10 (AAU01205, AAU01206).

In ovel human sequences for CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF) kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11.

They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polymucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal
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ce= "Casein kinase II phosphorylation site"
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857...859
/note= "Protein kinase C phosphorylation site"
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//note= "casein kinase II phosphorylation site" 802..147
//note= "Guanylate kinase (GUK) domain"
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e= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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/note= "Casein kinase II phosphorylation
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e= "N-myristoylation site"
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te= "Casein kinase II phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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581..684
/note= "Casein kinase II phosphorylation site"
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869..872
/note= "Casein kinase II phosphorylation site"
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754..756
/note= "Protein kinase C phosphorylation
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e= "Casein kinase II phosphorylation
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te- "Casein kinase II phosphorylation
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ce= "Casein kinase II phosphorylation
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te= "Casein kinase II phosphorylation
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te= "Casein kinase II phosphorylation
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ote= "Protein kinase C phosphorylation
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:e= "Casein kinase II phosphorylation
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== "Protein kinase C phosphorylation
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868..870
/note= "Protein kinase C phosphorylation
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ce= "Casein kinase II phosphorylation
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te= "Protein kinase C phosphorylation
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te= "Casein kinase II phosphorylation
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te= "Casein kinase II phosphorylation
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te= "Tyrosine kinase phosphorylation
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e= "Guanylate kinase (GUK) domain"
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e= "N-glycosylation site"
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+e≖ "MAGUK domain"
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mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical traials, and therapy (treatment and prophylaxis). The modulate it. CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation. cancer, NF kappab signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                              Gaps
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                                                                                                                                                                                  Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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te= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site"
                                                                                                                     Length 1147;
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:e= "Tyrosine kinase phosphorylation site"
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ce= "Casein kinase II phosphorylation
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te= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Protein kinase C phosphorylation
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                                                                                                                                           Indels
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230..251
/note= "Leucine zipper homology region"
                                                                                                                                                                                                                                                                                                                                                                         Human caspase recruitment domain, CARD-10 polypeptide.
                                                                                                                   Query Match 48.2%; Score 270; DB 22; Best Local Similarity 51.5%; Pred. No. 4.3e-26; Matches 51; Conservative 22; Mismatches 26;
                                                                                                                                                                                                                             DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
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te= "Coiled coil domain"
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                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis;
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from a human skin cDNA library. Also described are novel human sequences from a human skin cDNA library. Also described are novel human sequences for CARD-10. The polynucleotide encoding this sequence was isolated from a human skin cDNA library. Also described are novel human sequences care to CARD-10 and CARD-11 interact with Ecl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzhehmer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
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.885
== "Casein kinase II phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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1028..1031
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/note= "Casein kinase II phosphorylation site"
                                                     "N-myristoylation site"
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                                                                                        "Amidation site
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2000US-0513904
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1022..1024
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1021..1026
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                    /note= "C
893..898
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25-FEB-2000;
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The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal call carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal
                                                                                                                                                                                                                                 Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Maxos disease; extramammary Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acantholysis, Grover's disease, Hailey-Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73245-AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
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Pred. No. 5.6e-23;
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                                                                                                                                                                                                      Human plakoglobin interacting protein #3.
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                                                                                                AAU73247 standard; Protein; 1032 AA
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                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonne S,
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Length 1032; Indels

43.9%; Score 246; DB 22; 48.9%; Pred. No. 5.6e-23;

21; Mismatches

Conservative

Query Match Best Local Similarity Matches 46; Conserv

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DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65

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Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                                                                                                                                                                                                                                                               "CAMP- and cGMP-dependent protein kinase phosphorylation pite"
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phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
483..486
                                                                                                                                                                                                                                                     "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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267..270
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te- "Casein kinase II phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ..183
te- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cysteine rich repeat homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Indole-3-glycerol phosphate synthase homology region"
                                                                                  recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                  ..416
re- "Coiled coil domain"
                                                                                                                                                                                                             "CARD domain"
                                                                                                                                                                   Location/Qualifiers
                    AAU01204 standard; Protein; 536 AA
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23..26
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92..95
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197..21
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                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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RESULT 6
AAU01204
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The present sequence represents novel rat caspase recruitment

domain, CARD-9. The polynucleotide encoding this sequence was

solded from a rat neuronal DNA library. Also described are novel

thuman sequences for CARD-9, CARD-10 and CARD-11 (AAU01205-AAU01207).

CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought

CC cARD-9, CARD-10 and CARD-11 which is thought

CC cARD-9, CARD-10 and CARD-11 The sequences

CC cativity of CARD-9, CARD-10, or CARD-11. They can be used for

the internation can be used for treating a disorder associated

with abnormal levels of apoptosis by modulating the expression

CC or activity of CARD-9, CARD-10, or CARD-11. They can be used for

the treatment of hyperproliferative disorders (e.g. cancer),

autoimmune disorders (e.g. systemic lupus erythematosus), neurological

cultivity of alsease), and viral infection (e.g. HIV). The CARD polypeptide,

CC choin's disease, and viral infection (e.g. HIV). The CARD polypeptide,

CC choin's disease, and an antibody which selectively binds to CARD can be

cused in screening and detection assays (e.g. chromosomal mapping, tissue

typing, predictive medicine (prognostic assays, monitoring clinical

crials, and therapy (treatment and prophylaxis). The CARD polypeptide may

be used to screen for drugs that bind to and/or modulate it. CARD

crials, and therapy (treatment and prophylaxis).

Crials, expapab signalling, stress-related response and apoptosis in human

disease. A host cell containing a polynucleotide encoding CARD can be

cused to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                           /note="N-glycosylation site"
526..529 .
/note="Casein kinase II phosphorylation site"
7note="Casein kinase II phosphorylation site"
/note="Casein kinase II phosphorylation site"
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         7.00.c.
514..516
/hote= "Protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site"
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; Pred. No. 1.5e-19;
17; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                         "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig 1A-1B; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.8%;
Best Local Similarity 45.5%;
Matches 45; Conservative 1
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2000US-0513904.
                                                                                                                                                                                                                                                                                                   01-DEC-2000; 2000WO-US32716
                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0685791
                                                                                           ..527
                                                                           /note=
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N-PSDB; AAS05386.
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                                                                                                                                                                                                                            WO200140468-A2
                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                         03-DEC-1999;
18-FEB-2000;
25-FEB-2000;
                   Modified-site
                                                       Modified-site
                                                                                           Modified-site
                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2000;
                                                                                                                                                                                                                                                                  07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bertin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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antipositatic; antipositic interpolation of troop of control control of contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                             Human ORFX ORF831 polypeptide sequence SEQ ID NO:1662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 1326; 5507pp; English.
                                                          AAB41067 standard; Protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-602362/57.
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                                                                                                                              AAB41067;
RESULT 7
                              AAB41067
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(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX treating at yaven in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune defliciencies and disorders, infectious
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes substantially purified human proteins
                                                                                                                                                                    71 NDDECWNVLEGFRVTLTSVIDPSRITPYLRQCKVLNPDDEEQVLSDPNLVIRKRKVGVLL 130
                                                                                          Gaps
                                                                                                                                6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
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0
                                                      Length 174;
                                                                                          Indels
                                                                                          39;
                                                                                                                                                                                                                                  DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                      DB 21;
                                                    Score 209; DB 21;
Pred. No. 3.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX protein sequence SEQ ID NO:21546.
                                                                                          16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                ABP10782 standard; Protein; 174
                                                      37.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US10836
                                                                          44.48;
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                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-106308/14.
                                                      Query Match
Best Local Similarity
                174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myasthenia gravis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                          44;
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                  Sequence
                                                                                              Matches
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            arthritis, autoimmune thyroiditis, myasthenia gravis, graft versus host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an Oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                         primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                     37.3%; Score 209; DB 23; Length 174; 44.4%; Pred. No. 3.5e-19; Live 16; Mismatches 39; Indels
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, Otsuki '
                                                                                                                                                                                                                                                                                                                                                                                            DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
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T, Wakamatsu A, Nagai K,
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                     Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                   174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                    N.B.
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             complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13632 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
 an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CAMP- and cGMP-dependent protein kinase phosphorylation site"
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//note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                              Length 366;
                                                                                                                                                                                                                                                                                                          ; Score 209; DB 22; Length 3; Pred. No. 1e-18; 16; Mismatches 39; Indels
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/note= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Casein kinase II phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human caspase recruitment domain, CARD-9 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|: | | :||||||: | :| || :| || || || DILQRTGHKGYVAFLESLELYYPQLYKKVTGKEPARVFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                           DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
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te= "Coiled coil domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CARD domain"
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                                                                                                                                                                                                                                               of the present invention.
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Best Local Similarity
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The present sequence represents novel human caspase recruitment domain, CARD-9. The polynuclectide encoding this sequence was isolated from a human megakaryocyte CDNA ilbrary. Also described are novel human sequences for CARD-10 and CARD-11 (AAU01206, AAU01207) and rat CARD-9 (AAU01204). CARD-10 and CARD-11 interact with Bel-10 which is thought to activate nuclear factor (NF) kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, CARD-9, CARD-10, as immunogens, and in screening
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/note= "cAMP- and cGMP-dependent protein kinase
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/note=""\myristoylation site"
/note=""Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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ce= "Casein kinase II phosphorylation site"
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                                                                                                   "Cysteine rich repeat homology region"
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2000US-0507533.
2000US-0513904.
2000US-0685791.
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N-PSDB; AAS05387.
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cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disor (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappas signalling, stress-related response a apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
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Darier's disease; ectodermal dysplasia; skin fragility syndrome
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44.4%; Pred. No. 1.7e-18;
tive 16; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human plakoglobin interacting protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 42-43; 98pp; English.
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N-PSDB; AAS98201.
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nes 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICK; mouse; RIP-11ke interacting CLARP kinase; apoptosis regulator; ARC; caspase-1; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
interfere with the interaction of the polypeptide with plakoglobin The plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramamnary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey-Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73254 AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
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Best Local Similarity 51.49
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                        237 AA;
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activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used and cardiac disorders, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disorders, antistic antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the mouse CIPER protein. The invention relates to the human RICK (RIP-like interacting CLARP kinase) protein. The RICK protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RICK; mouse, RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease;
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                   4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
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8
                                                                                                                                                                                                                                                           14.5%; Score 81; DB 21; Length 233; 36.5%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY59413 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse CIPER protein sequence.
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N-PSDB; AAZ48768.
                                                                                                                                                                                                                                                                            Local Similarity
les 31; Conser
                                                                                                                                                                                                                       233 AA;
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and DREP-1) RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking ODS5-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anemia, ischaemic injury, and toxin-induced liver of disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.
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tive 14; Mismatches 33; Indels
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11-JUL-2000; 2000US-0614150
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nes 30; Conserv
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                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
     and
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                             2 LTALDEETLWE----MMESHR-----HRIVRCICPSRLTP--YLRQAKVLCQLDEEEV 48
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                            Length 845;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                   (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                               DB 22;
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                                                                                                                                                                                                                                                                                                                      Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                            12.6%; Score 70.5; 30.7%; Pred. No. 6.
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Chimeric - Unidentified.
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The invention relates to an immunogenic complex comprising one glycoside and one lipid, integrated into an iscom complex or matrix and one antigen which is integrated into the iscom complex or coupled on to or mixed with the iscom complex or iscom matrix complex, also comprising an enzyme. The immunogenic complex is used for providing iscom complexes on to which a receptor expressed on a cell capable of antigen presentation. The complex may also be used as an immunogenic matrix complex compression on a cell capable of antigen presentation. The proteins, which specifically bind to a receptor expressed on a cell capable of antigen presentation have been coupled. The invention is used as vaccine. The present sequence is cholera toxin Al subunit (CTAI).OVA
                                                                                                                                                                                                                                                                                                                       immunostimulating complexes (iscoms) and a lipid integrated into the
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-36-296B-61
US-08-506-296B-61
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US-09-031-485-15
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Sequence 36, Application US/09069023A

Patent No. 6348573

GENERAL INFORMATION:
APPLICANT: Innez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Roseki, Takeyoshi
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT PILLING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
ILBRITELLING DATE: 233
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Sequence 38, Application US/09069023A

Patent No. 6348673

GENERAL INFORMATION:
APPLICANT: Inohara, Machiro
APPLICANT: Inohara, Nachiro
APPLICANT: ROSeki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION UNMBER: US/09/069,023A
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAGHLIDILKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
    TYPE: PRT CRGANISM: Homo sapiens US-09-069-023-36
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US-08-727-126-2
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                                                                                                                                                                                                                                                                                                                                                                                                                4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
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APPLICANT: Duhamel, Gerald E.
APPLICANT: Elder, Robert
TITLE OF INVENTION: Nucleotide Sequences and Methods for
TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5698394west Center
CITY: Minneapolis
STREET: MN
COUNTRY: USA
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                                                                                                                                                                                                                           13.9%; Score 78; DB 4; Length 233; 35.3%; Pred. No. 0.015; tive 14; Mismatches 33; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,492
FILING DATE:
CLASSIFICATION: 424
ATTONNEY/AGENT INPORMATION:
NAME: ROWALCHYK, Ratherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/POCKET NUMBER: 9338.25US01
TELECOMMULICATION INFORMATION:
TELECOMMULICATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 RAGKLLDYLQ-ENPRGLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08252492 Patent No. 5698394
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 497 amino acids
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Matches 24; Conservative
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.3%
Matches 30; Conservative
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                                               TYPE: PRT
COGANISM: Mus musculus
US-09-069-023-38
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TOPOLOGY: linear
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              LENGTH: 233
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RESULT 4

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US-08-942-761-2
US-08-942761
; Sequence 2, Application US/08942761
; Patent No. 6068843
; GENERAL INFORMATION:
; APPLICANT: Duhamel, Gerald E.
; APPLICANT: Elder, Robert
; TITLE OF INVENTION: Nucleotide Sequences and Methods for TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
                                         GENERAL INFORMATION:
APPLICANT: Duhamel, Gerald E.
APPLICANT: Duhamel, Robert
APPLICANT: Elder, Robert
TILE OF INVENTION: Nucleotide Sequences and Methods for
TITLE OF INVENTION: Detection of Serpulina Hyodysenteriae
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5869630west Center
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,126
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
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; Pred. No. 1.8;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 ----LLIYREKTNASIVLKDAVSFLMHENDIY 419
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6068843west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,492
FILING DATE: 01-JUN-1994
ATTORNEY,AGENT INFORMATION:
NAME: Kowalchyk, Katherine M.
REGISSPRATION NUMBER: 36,848
REFERENCE,DOCKET NUMBER: 36,848
TELECOMMUNICATION INFORMATION:
Sequence 2, Application US/08727126
Patent No. 5869630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.9%;
26.1%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 612-332-5300
612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rrpE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-727-126-2
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            STREET: 3100 No. CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserve
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ZIP: 55402
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CITY: Cleveland
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US-08-427-497E-18
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                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.9%; Score 66.5; DB 3; Length 497; Best Local Similarity 26.1%; Pred. No. 1.8; Matches 24; Conservative 18; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08341843B
Patent No. 587225
GENERAL INFORMATION: Vance
APPLICANT: Lemmon, Vance
TITLE OF INVENTION: Nucleotide Sequence of LICAM and
PATEL OF INVENTION: Nucleotide Sequence
TITLE OF INVENTION: The Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: 1100 Superior Avenue
STREET: Objo
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/942,761
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURREIL ASCII
CURREIT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,843B
FILING DATE: NO. 5872225ember 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 ----LLIYREKTNASIVLKDAVSFLMHENDIY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 HLLDLLKTRGK-NGAIAFLESLKF--HNPDVY 91
                                                                                                                                                                                                                                                                                                                                        9338.250S01
                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,492
FILING DATE:
ATORNEY, AGENT INFORMATION:
NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 9338.250
TELECOMMUNICATION INFORMATION:
TELECHOME: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 497 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-341-843B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-942-761-2
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41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Method for Characterizing the Nucleotide Sequence of LICAM and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08427497E
Patent No. 5969124
GENERAL INFORMATION: Vance
TITLE OF INVENTION: Nucleotide Sequence of LIC;
Patent No. 5969124
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: the Nucleotide Sequence
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: mouse INDIVIDUAL ISOLATE: 8 day old mouse brain IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         member of the immunoglobulin
superfamily with binding domains
similar to fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neural adhesion molecule L1 is a
                                                                                REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELERX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minitch & McKee
STREET: 1100 Superior Avenue
STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: lamda GT 10 and lamda GT11
CLONE: synthesis of several clones
PUBLICATION INFORMATION:
FILING DATE: June 26, 1992
ATTORNEY/AGENT INPORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: amino acids
HYPOTHETICAL: irrelevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Tacke, R.
AUTHORS: Scherer, H.
AUTHORS: Teplow, D.
AUTHORS: Fruh, K.
AUTHORS: Schachner, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Conservative
                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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65 NLNPDLQY 72
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GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TILLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
Patent No. 6313265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS: 77
CORRESPONDENCE ADDRESS: 78
STREET: 1050 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 COLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGALAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 65.5; DB 4; Length 209; 27.9%; Pred. No. 0.69; tive 12; Mismatches 26; Indels 1.
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STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FITTING, Thomas
REGISTRATION UNDRER: 34,163
REFERENCE/COCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 61:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 27.9%
Matches 19; Conservative
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; FRAGMENT TYPE: internal
US-08-506-296B-61
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MEDIUM TYPE: Floppy
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STATE: California
                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                          92037
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                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: mouse
INDIVIDUAL ISOLATE: 8 day old mouse brain
INDIVIDUAL ISOLATE: 1 day old mouse brain
LIBRARY: lamda GT 10 and lamda GT11
CLONE: Synthesis of several clones
PUBLICATION INFORMATION:
AUTHORS: Moos, M.
                                           COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neural adhesion molecule Ll is a
member of the immunoglobulin
superfamily with binding domains
similar to fibromectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CWR 2 149-3-1
                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,497E
FILING DATE: APPLI 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/491
FILING DATE: June 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-3-
TELECHONICATION INFORMATION:
TELECHONICATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-506-296B-61; Sequence 61, Application US/08506296B
                                                                                                                                                                                         COMPUTER: Compag Prolinea 5100e OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: amino acids HYPOTHETICAL: irrelevant ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scherer, H.
Teplow, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tacke, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLUME: 334
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701-703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
AUTHORS:
TITLE: Ne
TITLE: me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: S. JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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192 MRGCRHSGVRIIIPPRKAP--QPTRVTCRYLGKDKLAHPPPLSEGEALASRILEMAPHGA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/09031485

Patent No. 5824306

GENERAL INFORMATION:
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85

CORRESPONDENCE SI
ADDRESSEE: CACAI TAILKINGTON Verser, Ph.D.
ADDRESSEE: CACAI TAILKINGTON
ADDRESSEE: ACAICAI TAILKINGTON
ADDRESSEE: CACAI TAILKINGTON
ADDRESSEE: THOSK COLPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.7%; Score 65.5; DB 2; Length 409;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches 33; Indels 2:
                                                                                                                                                        DB 4; Length 397;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR.1997
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                      11.7%; Score 65.5; DE 27.9%; Pred. No. 1.8; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 15:
                                       // TOPOLOGY: linear
MOLECULE TYPE: protein
// FRAGMENT TYPE: C-terminal
US-08-506-296B-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 amino acids
                                                                                                                                                                              Best Local Similarity 27.98
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
          amino acid
                                  linear
                                                                                                                                                                                                                                                                                                                                                            96 GLQPDVDF 103
                                                                                                                                                                                                                                                                                                                                                                                                           118 NLNPDLQY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-031-485-15
                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Cunningham, Bruce A.
APPLICANT: CUNDANTION: UNURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 1051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.7%; Score 65.5; DB 4; Best Local Similarity 27.9%; Pred. No. 1.2; Matches 19; Conservative 12; Mismatches 26;
                                                                                                                                                                                                   NAME: Fitting, Thomas
RECISTRATION UNDBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 488.0
TELECOMMUNICATION INFORMATION:
TELEFAX: (19) 554-6312
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acids
                                                                                                 APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/08506296B Patent No. 6313265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION UNDBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 amino acids
                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADULE.
STREET: 1000CCTTY: La Jolla
STATE: California
  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GLQPDVDF 103
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US-08-506-296B-59
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                                                       SOFTWARE:
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192 MRGCRHSGVRIIIPPRKAP--OPTRVTCRYLGKDKLAHPPPLSEGEALASRILEMAPHGA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Liang
Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
USES THEREOF
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 65.5; DB 3; Length 409; illarity 25.0%; Pred. No. 1.9; Conservative 12; Mismatches 33; Indels 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carol Talkington Verser, Ph.D. Heska Corporation
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 KFLGPVILEVPHFASLRGREREIVILRS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                           HW-5-C1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-557-034-15; Sequence 15, Application US/09557034; Patent No. 6365569 EBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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nes 22; Conserva
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                                                                                                STATE: CC
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                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
APPLICANT: Blahm, E. Soot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Colins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 409;
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US-09-065-474-15
Sequence 15, Application US/09065474
Faquence 15, Application US/09065474
Fatent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
APPLICANT: Belm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: WordPerfect
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/847,429A
FILLING DATE: 24.APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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11.7%; Score 65.5; DB
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches
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                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435 ATTORNEY AND CLASSIFICATION: NAME: VERSEY, CATOL Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: HW-5 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272 TELEFAX: 970/484-9505
                                                                                                                                                                        Sequence 15, Application US/08847429A
Patent No. 5827692
                     : 409 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                            US-08-847-429A-15
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Sequence 18, Applisequence 8, Applisequence 10, Applisequence 2, Applisequence 20, Applisequence 4, Applisequence 200, Appliseq
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Sequence 230, App
Sequence 230, Appli
Sequence 285, App
Sequence 4, Appli
Sequence 3, Appli
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Sequence 5, Appli
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                                                                                                                                                                                                                                                                  (without alignments)
500.428 Million cell updates/sec
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                                                                                                                                                                                                                          January 22, 2003, 08:49:35; Search time 4.31452 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-767-215-2

US-10-032-159A-18

US-10-032-159A-8

US-10-032-159A-10

US-10-032-159A-2

US-10-032-159A-2

US-10-032-159A-2

US-10-032-159A-2

US-10-032-159A-4

US-10-032-159A-4

US-10-038-626-4454

US-10-078-929-200

US-10-078-929-200

US-09-771-161A-230

US-09-771-161A-230

US-09-771-161A-230

US-10-058-820-7

US-10-058-820-4

US-10-058-820-4

US-10-058-820-3
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560
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Listing first 45 summaries
                                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 236, Appl
Sequence 178, Appl
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Patent No. US20020164703A1

GENERAL INFORMATION:

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: DENCODING NUCLEIC ACIDS, AND METHODS OF USE

CURRENT PPLICATION NUMBER: US/10/032/159A

CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 560; DB 9;
100.0%; Pred. No. 3.5e-57;
tive 0; Mismatches 0;
US-09-992-598-236
US-10-989-233A-236
US-10-989-735-236
US-09-999-735-236
US-09-990-444-236
US-09-990-436-236
US-09-990-436-236
US-09-990-436-236
US-09-991-681-236
US-09-991-681-236
US-09-991-681-236
US-10-175-731-178
US-110-175-731-178
US-110-175-731-136
US-09-989-723-236
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US-09-989-723-236
US-09-989-723-236
US-09-989-723-236
US-09-989-732-236
US-09-989-732-236
US-09-999-732-236
US-09-999-732-236
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US-09-999-732-236
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US-09-991-1163-236
US-09-991-1163-236
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-032-159A-16
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ORGANISM: Homo sapiens
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 NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                   US-10-032-159A-16
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Best Local Simi
Matches 107;
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RESULT 2 US-09-767-215-2

Sequence 11, Appl

US-09-910-150-11

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US-10-032-159A-10
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US-10-032-159A-8
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                                  GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1004
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US-09-767-215-5
; Sequence 5, Application US/09767215
; Sequence 5, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-142001
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; PRIOR FILING DATE: 2000-02-09
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100.0%; Pred. No. 5.1e-56;
iive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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Sequence 2, Application US/09767215 Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 107; Conservative
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Best Local Similarity 100.
Matches 107; Conservative
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CORGANISM: Homo sapiens
US-09-767-215-5
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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; GENERAL INFORMATION:
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
; TITLE OF INVENTION: CARD-DOMAIN CALDS, AND METHODS OF USE
; FILE REFERENCE: P-LJ 5100
; CURRENT APPLICATION NUMBER: US/10/032/159A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-21
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APPLICANT: GOdZik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
FITLE OF INVENTION: BNCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-L3 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT APPLICATION NUMBER: US/10/032,159A
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 1247;
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Best Local Similarity 51.5%; Pred. No. 1e-22;
Matches 51; Conservative 22; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 484; DB 9; 100.0%; Pred. No. 1.1e-48; rative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                              LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                          LENGTH: 366
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APPLICANT: Pawlowski, Krzysztof
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Radin C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCOING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-19
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REPERBENCE: P-LJ 5100
CURRENT APPLICATION UNMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR PAPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SSOTTWARE: FastSEQ for Windows Version 4.0
LENGTH: 92
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Petent No. USF2020164703A1
GENERAL INFORMATION:
APPLICANT: Read, John C.
APPLICANT: Read, John C.
APPLICANT: Read, John C.
APPLICANT: ROGAIL, Adam
ITILE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
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44.4%; Pred. No. 2.1e-16;
tive 16; Mismatches 39;
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53.3%; Pred. No. 1.2e-22;
tive 20; Mismatches 22;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 366
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; Patent No. US20020164703A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.3
Matches 48; Conservative
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; ORGANISM: Homo sapiens
US-10-032-159A-10
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Patent No. US20020164703A1
Sequence 4, Application US/10032159A
Patent No. US20020164703A1
Seberarl Information:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: EMCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
ENCODING NUCLEIC ACIDS, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                      37.3%; Score 209; DB 9; Length 366;
44.4%; Pred. No. 2.1e-16;
tive 16; Mismatches 39; Indels
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                    FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGANA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO:
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%
Best Local Similarity 44.4%
Matches 44; Conservative
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62 HKGYVAFLESL 72
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APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Stress Response
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT APPLICATION NUMBER: US/266,394
PRIOR PILING DATE: 2000-05-05
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-05-07
PRIOR PELING DATE: 1999-05-11
PRIOR PELING DATE: 1999-05-11
PRIOR PELING DATE: 1999-05-11
PRIOR PELING DATE: 1999-05-11
PRIOR PELICATION NUMBER: 60/13343
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR PELICATION NUMBER: 60/13348
PRIOR FILING DATE: 1999-05-11
PRIOR PELICATION NUMBER: 60/13348
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PRIOR PELICATION NUMBER: 60/13346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.1%; Score 67.5; DB 9; Length 763; Best Local Similarity 30.4%; Pred. No. 9.1; Matches 21; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                               FILE REFERENCE: 249-125
CURRENT APPLICATION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PACENTIN VET: 3.0
SSOFTWARE: PACENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4454
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Falco, Saverio Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Famodu, Omolayo O.
Odell, Joan T.
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Thorpe, Catherine
Weng, Zude
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakai, Hajime
                                                                                                                                                                                           OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 LVTGLQPDV 101
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APPLICANT:
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APPLICANT:
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APPLICANT: Schense, Jason
APPLICANT: Lisch, Andreas
APPLICANT: Lisch, Andreas
APPLICANT: Lisch, Andreas
APPLICANT: Lisch, Andreas
APPLICANT: Hall, Helke
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP
CURRENT APPLICATION NUMBER: US/10/024,918
NUMBER OF SEQ ID NOS: 33
SOFTRANE: Patentin version 3.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: (516)..(604)
COTHER INFORMATION: the sixth Ig-like domain of the cell adhesion molecule L1
US-10-024-918-27
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                                                                                                                                                                                                                                                                          7 EETLWEMMESHRHRIVRCICP-----SALTP----YLRQAK-VLC 41
                                                                                                                                                                                                                                                                                                                                                                     42 QLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTG----L 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 CQLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT 95
                                                                                                                                                                                                                                  36;
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Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 80262-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILLING DATE: 2001-01-26
                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.7%; Score 65.5; I Best Local Similarity 27.9%; Pred. No. 29; Matches 19; Conservative 12; Mismatches
                                                                                                                                                                                     Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10024918; Patent No. US20020168718A1
                                                                                                                                                                                  12.0%;
24.6%;
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Mcrosoft Office 97
SEQ ID NO 200
LENGTH: 431
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey
                                                                                                           ; ORGANISM: Ipomoea batatas
US-10-078-929-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1260
TYPE: PRT
ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 SPNLNINSWT 370
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 32; Conserv
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981 NLNPDLQY 988
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US-09-771-161A-229
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                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 HKDIKPGNL--LLTTGGTLKISDLGVAEALHPFAADDTCRTSQGSPAFQPPEIANGLDTF 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                6 DEETLWEMMESHRHRIVRCIC-----PSRLTPYLRQAKVLCQL-DEEEVLHSPRLT 55
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                                                                                                                                                                                                                                                                                                                                 Query Match 11.2%; Score 63; DB 10; Length 433; Best Local Similarity 21.0%; Pred. No. 15; Matches 30; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.2%; Score 63; DB 10; Length 433; 21.0%; Pred. No. 15; tive 19; Mismatches 36; Indels
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PAPLICANTE. LEVELUE, et al.,

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802602-0005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 13676

PRIOR FILING DATE: 2000-011-28

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 273

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 NSAMRAGHLLDLLKTRG--KNGAIAFLESL----
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-16-15
PRIOR FILING DATE: 2000-6-15
PRIOR PILING DATE: 2000-6-15
PRIOR PILING DATE: 2000-6-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-771-161A-230
Sequence 230, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGFKVDIWSAGVTLYNITTGLYP 254
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Best Local Similarity 21.0%
Matches 30; Conservative
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; ORGANISM: Homo sapiens
US-09-771-161A-230
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-771-161A-229
                                                                                                                                                                                                                                         TYPE: PRT
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| Sequence 7, Application US/10058820
| Patent No. US2002015547941
| GENERAL INFORMATION:
| APPLICANT: Bogan, Jonathan S.
| APPLICANT: Lodish, Harvey F.
| TITLE OF INVERTION: Expression Cloning Method
| FILE REFERENCE: 0399-2025-002
| CURRENT FILING DATE: 2001-06-17
| PRIOR FILING DATE: 2001-06-18
| PRIOR FILING DATE: 2001-01-26
| PRIOR FILING DATE: 2001-01-26
| SOFTWARE: FastSEQ for Windows Version 4.0
| SOFTWARE: PastSEQ for Windows Version 4.0
| SOFTWARE: PRIOR PRIOR DATE: 2001-01-26
| SOFTWARE: PRIOR DATE: 2001-01-26
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January 22, 2003, 08:49:35 ; Search time 8.19758 Seconds (without alignments) 1254.807 Million cell updates/sec Run on:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SUMMAKIES	ID		<b>Н97280</b>	S59644	T33012	D72349	T50952	T26673	E86922	T13018	AB0269	D95365	H70947	E83849	S05479	E69264	H83493	875969	T39654	A41333	T33951	AB3375	S27802	T19450	H72623	YRHUB6	A30227	AD2318	AF2130	
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	Length	210	265	1583	265	522	270	315	460	1446	521	853	448	496	1260	320	532	554	618	221	234	299	2150	2150	235	537	263	297	349	
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	Score	73	73	72.5	71	69.5	67.5	67.5	67.5	29	66.5		ഹ	വ	65.5	4	4	4	4	64	64	64		64	63.5	m.	63	63	63	
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S57142	H70411	T44802	T09459	G83824	S13221	E82570	B70697	S69181	T31673	T01239	T15890	S36126	G97127	A89124	H64402
7	7	7	7	7	7	7	~	7	7	7	7	7	7	1	7
728	867	1025	1025	195	326	373	461	513	1036	1111	1168	1259	259	271	298
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11.2	11.2	11.2	11	11.	11.	11.	11.2	11.	11.2	11.2	11.2	11.2	11.1	11.1	11
63 11.2			63 11.3	62.5 11.3						62.5 11.2				62 11.	62 11.

## ALIGNMENTS

RESULT 1 S55671

	Gaps
	30;
Length 210;	24; Indels
 	24;
DB 2, 2, 5;	ches
e 73;	ismat
Scor	3; W
13.0%;	tive 1
nilarity	Conserva
ch 1 Sir	28;
Query Match 13.0%; Score 73; DB 2; L Best Local Similarity 29.5%; Pred. No. 2.5;	Matches

5

S	6	8		
Gap	EVL 4			
30;	GLDEEF	REDAE		
Indels	LROAKVLC	:    :      LDHLRAKKILSREDAEEV-		
24;	SRLTPY	HQT		
<pre>best Local Similarity 29.5%; Pred: No. 2.5; Matches 28; Conservative 13; Mismatches 24; Indels 30; Gaps</pre>		16 LTEEDIWDVERLCLEELRVLLVSHLKSHKHLDHLRAKKILSREDAEEV- 63	50 HSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLESLK 84	64 -SSRAT-SRSRAGLLVDMCQDHPR-GFQCLKESCK 95
Loca es	1.5	1 91	50 H	- 49
Match	QY	qq	δy	qq

Dydroxyethylthiazole kinase ThiM/ThiK (FS1) CAC3095 [imported] - Clostridium acetobut C. Species: Clostridium acetobutylicum C. Species: Accession: H97280 acetobutylicum C. Species: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001 R. Accession: H97280 acetobutyling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A. Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325 Acetobutylitum A; Residues: 1-265 <KUR> A; Residues: 1-265 <KUR> A; Residues: 1-265 <KUR> A; Residues: 1-265 <KUR> A; Cross-references: GB:AEO01437; PIDN:AAK81035.1; PID:915026160; GSPDB:GN00168 A; Experimental source: Clostridium acetobutylicum AFCC824

A;Gene: CAC3095 C;Superfamily: phosphomethylpyrimidine phosphate kinase

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A; Map position: 4
A; Introns: 7/2; 32/1; 114/3; 165/3; 202/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%;
28.4%;
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30.0%;
                                                                                                                                          12.7%;
23.9%;
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                       Similarity
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A;Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
                                                                                                                                          Query Match
Best Local Simi
Matches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
D72349
                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Reference number: 221731
A.Accession: T38603
A.Accession: T38603
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Roceule type: DNA
A.Residues: 1-1583 <DE2>
A.Cross-references: EMBL:250113; NID:9914878; PIDN:CAA90463.1; PID:9914883; GSPDB:GN0006
A.Cross-references: EMBL:250113; NID:9914878; PIDN:CAA90463.1; PID:9914883; GSPDB:GN0006
A.Cross-references: EMBL: Data Library, August 1998
A.Reference number: 222478
A.Accession: T43392
A.Accession: T43392
A.Accession: T43392
A.Accession: T4392
A.Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sister chromatid cohesion molecule Mis4p - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 18-Feb-2000 C; Accession: T38603; T43392; S59644 B; Par-1996 #text_change 18-Feb-2000 R; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF047658; PIDN:AAC04418.1; GSPDB:GN00022; CESP:K03H6.2
A;Experimental source: strain Bristol N2; clone K03H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
6
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C'Species: Caenorhabdalise alegans
Submitted to the EMBL Data Library, February 1998
A'Species on unaber: 221263
A'Species on unaber: 221263
A'Species on T33012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 LTKAGTATLME------IVPCLCSLFTRLNDYERLKKIVVSCLKSLEEARHS---ENN 1139
                                                                                                                                                                                                                                                        23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LTALDEETLWEMMESHRHRIVRCICP--SRLTPYLRQAKVL--CQLDEEEVLHSPRLTNS 57
                                                                                                        Gaps
                                                                                                                                                                                                 20 RIVRCICP--SRLTPYLRQAKVLCQL---DEEEVLHSPRLTNS-----AMRAGHLLD-L 67
                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%; Score 72.5; DB 2; Length 1583; 29.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 265;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: mis4; SPAC31A2.05c
A;Map position: 1
A;Introns: 33/1; 98/2; 543/3; 699/3; 1294/2; 1339/3; 1558/3
                                                                                                   29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 12.9%; Score /2.5; De Best Local Similarity 29.0%; Pred. No. 31; Matches 31; Conservative 14; Mismatches
13.0%; Score 73; DB 23.8%; Pred. No. 3.3; ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TDLFYKNGYIEWFKLEKIDNPNTH 208
                                                                                                                                                                                                                                                                                                                                                                                         68 LKTRGKNGAIAFLESLKFHNPDVY 91
         Query Match 13.0%
Best Local Similarity 23.8%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: K03H6.2
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-522 <ARNA
A;Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD35747.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: T50952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.H.; Hic
                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72349
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                      4;
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C;Date: 21.Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 EPLWKLTDEER-SFVRVYHPGKVTYINLEKDALLRAREEGILLSPEEINLHPEKHTMVAG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                            8 ETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTN----SAMRAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: TM0663
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-270 <SCH>
A; Residues: 1-270 <SCH>
A; Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.70
A; Experimental source: BAC clone B24P7; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 WEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLD--EEEVLHSPRLTNSAMR-
                                                                                                                                                                                                                       -----AGHLL-----DLLKTRGKNGAIAFLESLKFHNPDVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transposase related protein [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                      40;
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     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5; DB
Pred. No. 18;
16; Mismatches
                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67.5; 1
Pred. No. 13;
  DB
Score 71;
Pred. No. 5
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	- Arabidopsis thaliana a (mouse-ear cress) _revision 13-Aug-1999 #text_change 22-Oct-1999 1 Staveren, M.; Dirkse, W.; Stiekema, W.; Bancro: ance Database, July 1999 1 Staveren, M.; Dancro ance Database, July 1999 1 Columbia; BAC clone FBL21 1 Columbia; BAC clone FBL21 1 1221/3; 1289/2; 1330/3; 1399/3 1 FBC Columbia; BAC clone FBL21 1 Page 1 Page 2 Pa	SHRHRIVECI    :::     :::    EIRYPSIKCY   CLLKTRGKNG 	ABD0269 anthranilate synthase (EC 4.1.3.27) component I [imported] - Yersinia pestis (strain c. Species: Yersinia pestis C. Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001 C. Accession: ABD0269 R. Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M. Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel ATILE: Genome sequence of Yersinia pestis, the causative agent of plague. A.; Reference number: AB0001; MUD:21470413; PMID:11586360 A.; Status: preliminary A.; Accession: AB0269 A.; Status: Preliminary A.; Molecule type: DNA A.; Residues: 1-521 <kur> A.; Cross-references: GB:AL590842; PIDN:CAC91014.1; PID:g15980208; GSPDB:GN00175 C.; Genetics: A.; Genetics: A.;</kur>
Matches 24; Conservative 11; Mismatches 26; Indels 19; Gaps 4;  Qy 29 RLTPYLRQAKV	T26673  T26773  T26773  T26773  T26773  T2677  T26	Query Match  12.1%; Score 67.5; DB 2; Length 315;  Best Local Similarity 26.8%; Pred. No. 16;  Matches 30; Conservative 15; Mismatches 40; Indels 27; Gaps 5;  Qy 14 MESHRHRIVRCICPSRL-TPYLRQAKVLCQLDEEVLHSPRLTNSAMRAGHLLD 66  18 LAENRPEFQQAIADSPLFTAYMKLLKRQAELSPRILSALLSALSSIVRSHLPA 70  Qy 67 LLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSN 105	RESULT 8 E86922 Probable FAD-Linked oxidoreductase ML0109 [imported] - Mycobacterium leprae C.Species: Mycobacterium leprae C.Species: Mycobacterium leprae C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C.Accession: E86922 R.Cole, S.T.: Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HC R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001 A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, Mulbillands A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Simon, S.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schitcher, S.; Seeger, M.; Score 67.5; DB 2; Length 460; Schitcher, S.; Schitcher, S.; Schitcher, S.; Schitcher, S.; Score 67.5; DB 2; Length 460; Seeretics, A.; Conservative 10; Mismatches 35; Indels 63; Gaps 7; Matches 34; Conservative 10; Mismatches 35; Indels 63; Gaps 7; Matches 34; Conservative 10; Mismatches 35; Indels 63; Gaps 7; Db 163 TGKDSELFWATVGGNGLTGIMRATIEMM

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Cybere to a unsculus (house mouse)
Cybere is Mus musculus (house mouse)
Cybere is Mus musculus (house mouse)
Cybere in Superplay #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cybere in Specession: SO5479; B60850; S22167
Rymoos, M.: Tacke, R.; Scherer, H.; Teplow, D.; Frueh, K.; Schachner, M.
Nature 334, 701-703, 1988
A; Title: Neural adhesion molecule L1 as a member of the immunoglobulin superfamily wing A; Reference number: SO5479; MUD: 88318924; PMID: 3412448
A; Rocession: SO5479
A; Molecule type: mRNA
A; Residues: 1-1260 cMOO>
A; Cross-references: EMBL: X12875; NID: 953336; PIDN: CAA31368.1; PID: 953337
A; Note: part of this sequence including the amino end of the mature protein, was con R; Rathjen, E.G.; Wolff, J.M.; Frank, R.; Bonhoeffer, F.; Rutishauser, U.
J. Cell Biol. 104, 343-353, 1987
A; Title: Membrane qlycoproteins involved in neurite fasciculation.
A; Reference number: A60850; MUD: 87109457; PMID: 3805123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-496 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05316.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 20-28, XX',31-36 <RAT>
R;Koll, A.; Giese, K.P.; Mohajeri, M.H.; Montag, D.; Moos, M.; Schachner, M.
submitted to the EMBL Data Library, December 1991
A;Description: Analysis of promoter activity and 5' genomic structure of the neural
A;Reference number: S22167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillis halodurans
C;Species: Bacillis halodurans
C;Spaces: Dace-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E9849
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spore germination protein BH1597 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                               21; Gaps
                                                                                                                                                         5 LDEETLWEMMESHRHRIVRCICPSR-LTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 LTPYL-RQAKVLCQLDEE----EVLHSPRLTNSAMRAGHLLDLLKTRGKNGAIAFLES
                                                                                       11;
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    Length 448;
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                                                                                   Indels
                                                                              27;
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        5,
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        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. 45;
20; Mismatches
                                                                                   12; Mismatches
                                             40;
Score 65.5;
Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LKFHNPDVYTLVTGLQ---PDVDFS 104
        11.78;
31.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%;
27.1%;
        Query Match 11.7%
Best Local Similarity 31.5%
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                     |||:
|||09 LLDV----KNGA 206
                                                                                                                                                                                                                                                                                                                                    92
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                        64 LLDLLKTRGKNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: BH1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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D95365
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain G NuoG2 [imported] - Sinorhizobium m C; Species: Slnorhizobium meliloti
C; Species: Slnorhizobium meliloti
C; Species: Slnorhizobium meliloti
C; Species: Slnorhizobium meliloti
C; Decession: D95365
R; Barentt, M. J.; Fisher, R. F.; Jones, T.; Komp, C.; Abola, A. P.; Barloy-Hubler, F.; Bows
R; Brantet, M. J.; Fisher, R. F.; Jones, T.; Komp, C.; Abola, A. P.; Barloy-Hubler, F.; Bows
R; Raman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A; Reference number: A95562; MuID:21396509; PMID:11481432
A; Status: prelliminary
A; Molecule Lype: DNA
A; Residues: 1-853 < KND
A; Status: prelliminary
A; Cross-references: GB: EC006469; PIDN:AAK65486.1; PID:g14523958; GSPDB:GN00165
A; Cross-references: GB: EC006469; PIDN:AAK65486.1; PID:g14523958; GSPDB:GN00165
A; Cross-references: GB: Apola, A; Publer, A; Abola, P; Man, Cohie, P; Pinan, P; Cowie, A; Davis, R.W.; Dreano, S; Federspiel, N.A; Fisher, R.F.;
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 200,
A; Authors: Rahn, D; Rahn, M.L; Kalman, S; Reating, D.H; Kiss, E; Komp, C; Lelaure, heball, P; Vandehobi, M.; Vorholter, F. J.; Weidner, S; Wells, D.H; Word, K.; Yeh, K.A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Genetics:
A; Geneme: nucles plasmid
C; Keywords: oxidoreductase
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A;Experimental source: strain H37Rv
C;Genetics:
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Ficole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70947

A;Acc
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Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                ETL--LVLDHQHRSTR-LQASLFTPDSSEYQRLATRLEQLSHQLQQAPHPIPATSVPEMA 236
                                                                                               94
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                                                                                                                                                 --CQLDEEEVLHSPRLTNSAMRAGHLLDLLKTRGKN----GAIAFLESLKFHNPDVYTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 853;
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30.8%; Pred. No. ,c,
"" 12; Mismatches
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Best Local Similarity 30.8
Matches 16; Conservative
                                                                                                                                                                                                                                                             TGLQPDVDFSNF 106
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Purvate formate-lyase activating enzyme (act-1) homolog - Archaeoglobus fulgidus C; Species: Speci
A;Accession: $22167
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-165, L',167-189, 'E',191-281, 'S',283-395, 'S',397-514, 'APEKNPVDV',524, 'GEGNE
A;Cross-references: EMBL:X63511
C;Genetics:
A;Introns: 26/1; 31/1; 66/2; 133/1; 174/1; 231/1; 268/2; 330/1; 374/1; 422/1; 459/2
A;Note: the list of introns may be incomplete
C;Superfamily: neural cell adhesion molecule L; fibronectin type III repeat homology; if C;Reywords: alternative splicing; cell adhesion; duplication; glycoprotein; transmembran F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: neural cell adhesion molecule #status experimental <MAT>F;20-1260/Product: immunoglobulin homology <IRMI>F;20-1260/Domain: immunoglobulin homology <IRMI>F;31-592/Domain: immunoglobulin homology <IRMI
F;31-592/Domain: immunoglobulin homology <IRMI
F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 COLDEEEVLH-SPRLTNSAMRAGHLLDLLKTRGKNGAIAFLE----SLKFHNPDVYTLVT
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protein search, using sw model OM protein - January 22, 2003, 08:49:35 ; Search time 4.1707 Seconds (without alignments) 1064.082 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_10\_116 560 Title: Perfect score:

1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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McAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Be
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AGHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 116
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                                                                                                                                                                                                                                                                                                                           CARD. COIL (POTENTIAL).
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PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                   GUANYLATE KINASE.
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EMBL; AY03297; AAK54453.1; -.
EMBL; BC018142. AAH18142.1; -.
EMBL; BC001326; AAH01326.1; ALT_INIT.
INTERPRO; IPR000619; Guanylate_kin.
INTERPRO; IPR01478; PDZ.
SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ: 1.
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Matches 107; Conservative
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-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
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15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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743 QAQQQLLA -> HLLEDHRS (IN REF.
113496 MW; D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00595; PD2; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS502052; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 470; DB 1;
Pred. No. 1.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF363457; AAK60137.1; -. EMBL; BC004692; AAH04692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.9%;
85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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    (Carma 1).
    CARD11 OR CARMA1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
125
572
854
736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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m

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[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Carma 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa SI, Molt 4, A449 and G431 cells. Burkitt's Cortains: Contains I PDZ/DHR DOMAIN.
SIMILARITY: CONTAINS I DDZ/DHR DOMAIN.
SIMILARITY: CONTAINS I G18NNYLATE KINNSE-LIKE DOMAIN.
CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                           , Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; t. 505:198-198(2001).
                                                                            -:- FUNCTION: Activates NF-kappaB via Bc110 and IKK. Stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                        phosphorylation of Bcl10.
SUBUNIT: CARD11 and Bcl10 bind to each other by CARD-CARD
interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.2%; Score 270; DB 1; Length 1147; 51.5%; Pred. No. 5.1e-21; Live 22; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 442 COILED COIL (POTENTIAL).
673 748 PDZ.
966 1133 GUANYLATE KINASE.
808 808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PDZ; FALSE_NEG.
Coiled coil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF322641; AAG53402.1; -.
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51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00228; PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARD10 OR BIMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARA_MOUSE
P58660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Bimpl).
                                                               FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                        Gaide O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
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11D CARA_M
AC P58660
DT 15-JUN
DT 15-JUN
DT 15-JUN
DT 15-JUN
DT 16-JUN
DT 1
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                                                                                                                                      -- TISSIE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
--- SIMILARITY: CONTAINS 1 CARD DOMAIN.
--- SIMILARITY: CONTAINS 1 CARD DOMAIN.
--- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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09BW77; 09UGR5; 09UGR6; 09Y3H0;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EEDALWERIEGVRHRLTRALNPAKLTPYLRQCRVLDEQDEEEVLSTYRFPCRANRTGRLI 82
                                                   Benito A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.0%; Score 252; DB 1; Length 1021; 51.1%; Pred. No. 3.8e-19;
MEDLINE=21391892; PubMed=11387339; MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Be Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 AA; 114413 MW; 4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
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J. Biol. Chem. 276:21405-21409(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF363456; AAK60136.1; -. PROSITE; PS50209; CARD; 1.
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450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam or SMART.
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in no

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RAY MUDDIANE-LOUSTION; PROMES-LOUSTURE; RAY MEDLIANE-LOUSTION; PROMES-LOUSTURE; PROMES-LOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interaction. They both participate in a complex with MALTI, where MALTI binds to BellO (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

TISSUE SPECIFICITY: Detected in adult heart, kidney and liver; lower levels in intestine, placenta, muscle and lung. Also found in fetal lung, liver and kidney.

SIMILARITY: CONTAINS I CARD DOMAIN.

CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J., Carmal, a CARD-containing binding partner of Bcl10, induces Bcl10 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                        Jaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: Activates NF-kappaB via Bc110 and IKK.
-1- SUBUNIT: CARD10 and Bc110 bind to each other by CARD-CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                    MEDLINE=20057165; PubMed=10591208;
MEDLINE-21255663; PubMed-11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402:489-495(1999).
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                     SRRATUM.
                                                                                                                                                          Gaide O
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Ref.4 sequence differs from that shown due to various

gene identification problems.

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             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D.,
Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E.,
Distefano P.S., Alnemri E.S.; Du M.-Q., Dyer M.J.S., Robison K.E.,
CARD9 is a novel caspase recruitment domain-containing protein that
interacts with Bcl10/CLAP and activates NF-kappa B.";
J. Biol. Chem. 275-141082-41086(2000).
-!- FUNCTION: Activates NF-kappa via Bcl10 (By similarity).
-!- SUBUNIT: Self-associates. CARD9 and Bcl10 bind to each other by
CARD-CARD interaction (By similarity).
-!- SUBCELULLAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                 6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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 as its content is
                                                                                                                                                                                                                                                                                                                                Length 1032;
                                                                                                                                                                                                                                           Q -> R (IN REF. 4).

K -> K Q (IN REF. 4; CAB63075).

R -> L (IN REF. 4; CAB63075).

WW: 8377319AB82A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                                                                                                                                                               CARD.
COILED COIL (POTENTIAL).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                ; Score 246; DB 1;
; Pred. No. 1.7e-18;
21; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 9 (rCARD9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQP 99
non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                 43.9%; Score 246;
                                                                           EMBL; AY028896; AAK26165.1; -.
EMBL; AX032928; AAK54454.1; -.
EMBL; AL049851; CAB63075.1; ALT_SEQ.
EMBL; AL049851; CAB63076.1; ALT_SEQ.
EMBL; AL023315; CAB42832.1; ALT_SEQ.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
MEDLINE=20576268; PubMed=11053425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF311288; AAC28791.1; -. InterPro; IPR001315; CARD. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                  115946
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Best Local Similarity 48.5...
A6; Conservative
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                                                                                                                                                                                                1115
456
574
574
289
917
                                                                                                                                                                                               23 11
138 45
567 57
289 28
917 91
932 AA;
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                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoli T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Takiguchi S.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D., Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E., Distefano P.S., Alnemri E.S.; "CARD9 is a novel caspase recruitment domain-containing protein that lineracts with Bcll0/CLAP and activates NF-kappa B."; J. Biol. Chem. 275:41082-41086(2000).
                                                                                                                                                 6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                    Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. -:- FUNCTION: Activates NF kappaB via Bcl10. -:- SUBUNIT: Self-associates. CARD9 and Bcl10 bind to each other by
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                      .;
0
                                                                                        Length 536;
                                                                                                                      37; Indels
              CARD.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
6F33089CB7E6BAC9 CRC64;
                                                                                                                                                                                                             66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 9 (hCARD9)
CARD9.
                                                                                                      Pred. No. 1e-15;
                                                                                                                                                                                                                              536 AA
                                                                                                                    17; Mismatches
                                                                                        38.8%; Score 217; 45.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20576268; PubMed=11053425;
              98 CZ
277 CC
420 CC
62631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
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                                                                                                                      45; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
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TISSUE-Retinoblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalla; Eutheria;
              6
117
303
536 AA;
                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Coiled coil.
DOMAIN
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Q9H257; Q9F
                                            DOMAIN
SEQUENCE
                                                                                        Query Match
                               DOMAIN
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                                                                                                                      Matches
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Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P., Mattmann C., Tschopp J.;
Ratinann C., Tschopp J.;
Equine herpesvirus-2 E10 gene product, but not its cellular homologue, activates NF-kappaB transcription factor and c-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of vCARMEN)
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koseki T., Inohara N., Chen S., Carrio R., Merino J., Hottiger M.O., Nabel G.J., Nunez G.;
"CIPER, a novel NF kappaB-activating protein containing a caspase rectuitment domain with homology to Herpesvirus-2 protein E10.";
J. Biol. Chem. 274:9955-9961(1999).
                                                                                                                                                                                                                                                                                                                                                        6 DEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRAGHLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHE-218
                                                                                                                                                                                 COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
N -> S (IN REF. 3).
LSSGEPPEKER -> PAGLFGIGAVC (IN REF. 3).
GEB1835315B83DB5 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation) (BCD-10) (CED-3/ICH-1 prodomain homologous E10-like regulator) (CIPER) (CARD-CONTAINING molecule enhancing NFkappaB) (Cellular homolog of vCARME) (CELLULAR-ELO) (C-ELO) (CARD-Like apoptotic protein) (ACLAP).

BCL10 OR CIPER OR CLAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willis T.G., Jadayel D.M., Du M.-Q., Peng H., Perry A.R.,
Abdul-Rauf M., Price H., Karran L., Majekodunmi O., Wlodarska I.,
Pan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.S.;
"Bcll0 is involved in t(1:14)(p22;q32) of MALT B cell lymphoma and
mutated in multiple tumor types.";
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                       DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                      39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2] SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-41 AND GLY-78
                                                                                                                                                                                                                                                                                                                                                                                                                         66 DLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|: | | :|||||||: : | :| || || || DILQRTGHKGYVAFLESLELYYPQLYKKVTGKEPARVFS 104
                                                                                                                                                                                                                                                                         Score 209; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA.
                                                                                                                                                                                                                                                                                                                     16; Mismatches
              or send an email to license@isb-sib.ch).
                                             EMBL; AF311287; AAG28790.1; -.
EMBL; AK024001; BAB14766.1; ALT_FRAME.
EMBL; BC008877.1; -.
EMBL; BC008177; AAH08877.1; -.
Interpro; IPR001315; CARD.
PROSITE; P550209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                   CARD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lymphoma;
MEDLINE=99142601; Pubmed=9989495;
                                                                                                                                                                                                                                                    62267 MW;
                                                                                                                                                                                                                                                                                   37.3%;
                                                                                                                                                                                                                                                                                                      44.48;
                                                                                                                                                                                                                                                                                                                      44; Conservative
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                                                                                                                                                                 98
277
419
12
492
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                                                                                                                                                                                                                                                  536 AA;
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                                                                                                                                                                                                                                                                                                     3est_Local Similarity
                                                                                                                                                                   6
1117
332
12
482
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                                                                                                                                                   Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCLA_HUMAN
095999;
                                                                                                                                                                                                  DOMAIN
CONFLICT
                                                                                                                                                                                                                                                  SEQUENCE
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attributed to the Ig somatic hypermutation mechanism resulting in

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SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-28; LEU-41; ILE-46; LEU-47; GLU-53 AND ILE-55.
MEDLINE-99214590; PubMed=10187815;
Yan M., Lee J., Schilbach S., Goddard A., Dixit V.M.;
"mEl0, a novel caspase recruitment domain-containing proapoptotic molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS MALT LYMPHOMA SER-5; GLU-16; GLU-31; ARG-57; LYS-64; GLU-101; PRO-134; ALA-168; SER-174; GLU-213 AND ILE-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS MESOTHELIOMA SER-5; GLN-45; GLN-58; SER-93; VAL-153; GLU-213
                                                                                                                                                                         MEDLINE-99292766; PubMed-10364242; Srinivasula S.M., Ahmad M., Lin J.-H., Poyet J.-L., Fernandes-Alnemri T., Tsichlis P.N., Alnemri E.S.; "CLAP, a novel caspase recruitment domain-containing protein in the tumor necrosis factor receptor pathway, regulates NF-kappaB
                                                                                                                                                                                                                                                                                                                                  Costanzo A., Guiet C., Vito P.; "c-E10 is a caspase-recruiting domain-containing protein that interacts with components of death receptors signaling pathway and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apostolou S., de Rienzo A., Murthy S.S., Jhanwar S.C., Testa J.R.; "Absence of BCL10 mutations in human malignant mesothelioma."; Cell 97:684-686(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yul D., Yoneda T., Oono K., Katayama T., Imaizumi K., Tohyama M.;
"Interchangeable binding of Bcll0 to TRAF2 and cIAPs regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99251581; PubMed-10319863;
Zhang Q., Siebert R., Yan M., Hinzmann B., Cui X., Xue L.,
Rakestraw K.M., Naeve C.W., Beckmann G., Weisenburger D.D.,
Sanger W.G., Noworny H., Vesely M., Callet-Bauchu E., Salles G.,
Dixit V.M., Rosenthal A., Schlegelberger B., Morris S.W.;
"Inactivating mutations and overexpression of BCL10, a caspase recruitment domain-containing gene, in MALT lymphoma with
t(1.14)(p22:q32).";
Nat. Genet. 22:63-68(1999).
                                                                                                                                                                                                                                                                                                                                                                         activates nuclear factor kappaB.";
J. Biol. Chem. 274:20127-20132(1999).
                                                                                                                                 Biol. Chem. 274:10287-10292(1999)
                                                                                                                                                                                                                                                 activation and apoptosis.";
J. Biol. Chem. 274:17946-17954(1999).
N-terminal kinase.";
J. Biol. Chem. 274:9962-9968(1999).
                                                                                                                                                                                                                                                                                                       TISSUE=Spleen;
MEDLINE=99329013; Pubmed=10400625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [8]
PHOSPHORYLATION.
MEDLINE-21359851; PubMed-11466612;
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MEDLINE-99308628; Pubmed-10380921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 20:4317-4323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis signaling
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               Biol.
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         nucleotide transitions.
DISEASE: Defects in BCL10 are involved in various types of cancer.
SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTIG=VAR_013224.
S -> F (IN GERM CELL TUMOR, MESOTHELIOMA
AND OTHER CANCER CELL LINES).
                                                                                                                                                                                                                                                                                                Apoptosis; Chromosomal translocation; Anti-oncogene; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V -> I (IN MALT LYMPHOMA).
/FIId-VAR_013226.
L->A: ABOLISHES CELL DEATH-INDUCING CAPABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L -> S (IN MALT LYMPHOMA).
/FTId=VAR_013222.
MISSING (IN FOLLICULAR LYMPHOMA).
                                                                                                                                                                                                                                                                                                                               S (IN MALT LYMPHOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> E (IN MALT LYMPHOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=VAR_013212.
C -> R (IN MALT LYMPHOMA).
/FTIG=VAR_013213.
R -> G (IN GERM CELL TUMOR).
                                                                                                                                                                                                                                                                                                                                                                                   K -> E (IN MALT LYMPHOMA).

/FITG=VAR_013210.

K -> O (IN MESOTHELIOMA).

/FITG=VAR_013211.

T -> I (IN MESOTHELIOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId-vAR_013218.

S -> P (IN MALT LYMPHOMA).

/FTId-vAR_013219.

M -> V (IN MESOTHELIOMA).

/FTId-vAR_013220.
                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_013208.
V -> E (IN MALT LYMPHOMA).
/FTId=VAR_013209.
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D -> E (IN MALT LYMPHOMA).
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/FTId=VAR_013216.
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/FTId=VAR_013221.
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R -> Q (IN MESOTHELIOMA).
/FTId=VAR_013215.
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                                                                                                                                                                                                                                                                                                                                A -> S (IN MA MESOTHELIOMA)
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                                                                                                                                   EMBL, AJ006288; CAA06555.1; EMBL, AF057700; AAD15800.1; EMBL, AF100338; AAD16428.1; EMBL, AF127386; AAD32597.1; EMBL, AF105066; AAF06894.1; EMBL, AF08238; AAD24918.1; EMBL; AF08238; AAD24918.1;
                                                                                                                                                                                                                                                    InterPro; IPR001315; CARD.
Pfam; PF00619; CARD; 1.
SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                Genew; HGNC:989; BCL10.
                                                                                                                                                                                                                                                                                                                    101
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                                                                                                                                                                                                                                                                                                            Disease mutation.
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                                                                                                                                                                                                                                          MIM; 603517;
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                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABOLISHES NF-KAPPA-B ACTIVATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKK-IKAP complex (By similarity).
SUBUNIT: Self-associates by CARD-CARD interaction and interacts with other CARD-proteins such as CARD9, CARD10, CARD11 and CARD14.
Binds caspase-9 with its C-terminal domain (By similarity).
Interacts with TRAF2 and BIRC2/c-IAP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                  G->R: ABOLISHES NF-KAPPA-B ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
B cell lymphoma/leukemia 10 (B-cell CLL/lymphoma 10) (Bcl-10) (R-RCD1) (RCD).
                        ABOLISHES CELL DEATH-INDUCING
                                                   I->A: ABOLISHES CELL DEATH-INDUCING
                                                                      L->A: ABOLISHES CELL DEATH-INDUCING CAPABILITY.
                                                                                                     E->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                              I->A: ABOLISHES CELL DEATH-INDUCING
                                                                                                                                                                                Score 81; DB 1; Length 233;
                                                                                                                                                                                                        32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic (By similarity). PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 CARD domain.
             HOMO/HETERO-DIMERIZATION
                                                                                                                                                                                           0.16;
                                                                                                                                                                                                                                                                                                                                                                               233 AA
                                                                                                                                                                                                         14; Mismatches
                                                                                                                                           CAPABILITY
                                                               CAPABILITY
                                                                                                                 CAPABILIT
                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                    ||| ||| |: | :||::
| RAGKLLDYLQENPK-GLDTLVESIR 87
                                                                                                                                                                                                                                                                                     RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB016069; BAA88822.1; -
                                                                                                                                                                                14.5%;
36.5%;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                        41
                                                  46
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                                                                                                                            22
                                                                                                                                                      78
                                                                          47
                                                                                                                                                                                            Similarity
31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10116;
                        41
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                                                                                                                            22
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                                                                                                                                                                                                                                                                                                                                                                               BCLA_RAT
Q9QYN5;
                                                                                                                                                                                Query Match
                                                                                                                                                                                               Local
                                                                                                     MUTAGEN
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MUTAGEN
                         MUTAGEN
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q
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InterPro; IPR001315; CARD.

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SEQUENCE FROM N.A. MEDILIPE-92214545; PubMed=10187770; MEDILIPE-92214545; PubMed=10187770; Koseki T., Inohara N., Chen S., Carrios R., Merino J., Hottinger M.O., Nabel G.J., Nunez G.; "CIPER, a novel NF kappaB-activating protein containing a caspase reccuitment domain with homology to Herpesvirus-2 protein E10."; J. Baol. Chem. 274:9955-9961(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P.,
Mattman C., Tschopp J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation (BCI-10) (CED-3/ICH-1 prodomain homologous E10-like regulator) (mCIPER) (CARD-containing molecule enhancing NFkappaB) (Cellular homolog of vCARMEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Equine herpesvirus-2 ElO, but not its cellular homologue, activates NF-kB transcription factor and c-jun N-terminal kinase."; J. Biol. Chem. 274:9962-9968(1999).
                                                                                                                                                                                                                     4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                           MEDLINE-99142601; PubMed-9989495; Mills T.C., Jadayel D.M., Du M.-Q., Peng H., Perry A.R., Maldils T.C., Jadayel D.M., Du M.-Q., Peng H., Perry A.R., Abdul-Rauf M., Price H., Karren L., Majekodumi O., Wlodarska I., Pan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.S.; "Bcll0 is involved in t(1:14)(p22:q32) of MALT B cell lymphoma and cell 96:35-45(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yan M., Lee J., Schilbach S., Goddard A., Dixit V.M.;
millo, a novel caspase recruitment domain-containing proapoptotic
molecule.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (mE10)
                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CCARMEN) (Mammalian CARD-containing adapter molecule E10) (n(Cellular-E10) (c-E10) (CARD-like apoptotic protein) (mCLAP). BCL10 OR CIPER OR CLAP.
                                                                                                                                        Length 233;
                                                                                               SEQUENCE 233 AA; 25999 MW; B43274B4B825FC7D CRC64;
                                                                                                                                                                             32;
                                                                                                                                    14.5%; Score 81; DB 1; 36.5%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA
                                                                                                                                                                             Mismatches
                  SMART; SM00114; CARD; 1.
PROSTTE; PS50209; CARD; 1.
Apoptosis; Anti-oncogene; Phosphorylation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 274:10287-10292(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99214546; PubMed=10187771;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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TISSUE-Embryo;
MEDLINE-99214590; PubMed=10187815;
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MEDLINE=99292766; PubMed=10364242;
                                                                                                                                                                                                                                                                                                                        ||| ||| |: | | | :||:: | RAGKILDYLQENPK-GLDTLVESIR 87
                                                                                                                                                                                                                                                                                               60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                             14;
                                                                                                                                                                             31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
Pfam; PF00619; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                            BCLA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecule.
                                                                                                                                      Query Match
                                                                                                                                                             Best Local
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                      Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Promotes apoptosis, pro-caspase-9 maturation and activation of NF-KappaB via NIK and IKK. May be an adapter protein between upstream TNFR1-TRADD-RIP complex and the downstream NIK-
                                                                                                                                                                   INK-IKAP complex (By similarity).
SUBUNIT: Self-associates by CARD-CARD interaction and interacts with other CARD-proteins such as CARD9, CARD10, CARD11 and CARD14.
Binds caspase-9 with its C-terminal domain. Interacts with TRAF2 and BIRC2/c-IAP2 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
INTSSUE SPECIFICITY: Highly expressed in heart, brain, spleen, lung, liver, skeletal muscle, kidney and testis. Detected in developing brain, olfactory epithelium, tongue, whisker follicles, sallyary gland, heart, lung, liver and intestinal epithelia of stage 15 embryos.
PTM: Phosphorylated (By similarity).
Srinivasula S.M., Ahmad M., Lin J.-H., Poyet J.-L., Fernandes-Alnemri T., Tsichlis P.N., Alnemri E.S.; "CLAP, a novel caspase recruitment domain-containing protein in the tumor necrosis factor receptor pathway, regulates NF-kappaB activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ALDEETLWEM----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLTEEDLTEVKKDALENLRVYLCEKIIAERHFDHLRAKKILSREDTEEI--SCR-TSSRK 63
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C0539BC97102DBB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 1,
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sister chromatid cohesion protein mis4. MIS4 OR SPAC31A2.05C. Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; Anti-oncogene; Phosphorylation.
                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 CARD domain.
                                                   and apoptosis.";
J. Biol. Chem. 274:17946-17954(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 RAGHLLDLLKTRGKNGAIAFLESLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| ||| || || RAGKLLDYLQ-ENPRGLDTLVESIR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ006289; CAA06956.1; -. EMBL; AF057701; AAD15801.1; -. EMBL; AF100339; AAD16429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF127387; AAD32598.1; -. AF134396; AAD39148.1; -. BC024379; AAH24379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA; 25948 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1337994; BC110.
InterPro; IPR001315; CARD.
Pfam; PF00619; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.95
Best Local Similarity 35.35
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIS4_SCHPO
Q09725;
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01-NOV-1995
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MIS4_SCHPO
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A Squires Loyer Browner Labour Baker S., Basham D., Bowman S.,

Ray Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Ray Gouros J., Peat N., Hayles J., Basham D., Bowman S.,

Ray Brown D., Brown S., Chillingworth T., Churcher C.M.,

Ray Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Ray Goble A., Hamilan N., Harris D., Hiddigo J., Hodgson G.,

Ray Jones L., Jones M., Lather S., McDonald S., McLean J.,

Ray Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Ray Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Ray Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Ray Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Ray Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Ray Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Ray Heljens I., Vonckaert G., Aert R., Robben J., Grymonprez B.,

Ray Gabel C., Fuchs M., Fritzc C., Lehrach H., Reinhardt R., Pohl T.M.,

Ray Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Ray Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Ray Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Ray Lucas M., Rochet M., Gaillardin C., Pallada V.A., Galzon A., Thode G.,

Ray Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Ray Ray R., Cruzado L., Jimenez J., Sanchez M., Borsburg S.L.,

Ray Spakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Ray Ray R., Ray L., Barrell B.G., Nurse P.;

Ray Ray R., Ray 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATES WITH CHROMOSOMES IN A PUNCTARE FASHION THROUGHOUT THE CELL CYCLE. INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SIMILARITY: CONTAINS 5 HEAT REPEATS.
                                                                                                                                                                                                                                   Furuya K., Takahashi K., Yanagida M.;
Furuya K., Takahashi K., Yanagida M.;
"Faithful anaphase is snsured by Mis4, a sister chromatid cohesion
molecule required in S phase and not destroyed in G1 phase.";
Genes Dev. 12:3408-3418(1998).
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB016866; BAA74749.1; -- PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Repeat.
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HEAT
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                                                                                                                                                                                                        MEDLINE-99026114; PubMed-9808627;
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784
1034
                                        Schizosaccharomyces.
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1583
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C8CF2F1D5C3E9271 CRC64;

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                                                                                               2 LTALDEETLWEMMESHRHRIVRCICP--SRLTPYLRQAKVL--CQLDEEEVLHSPRLTNS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacieria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                   Length 1583;
                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADH dehydrogenase I chain G 2 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain G 2).
NUOG2 OR RAO828 OR SMA1523.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putnoky P., Jady B., Chellapilla K.P., Barta F., Kiss E.; "Rhizobium meliloti carries two sets of nuo genes."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      Indels
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                                                                                                                                                                                 58 AMRAGHLLDLLKTRGKNGAI----AFLESLKFHNP---DVYTLVTG
                   DB 1;
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TE; PS00198; 4FE4S_FEREDOXIN; 2.
TE; PS00641; COMPLEXI_75K_1; FALSE_NBG.
TE; PS00642; COMPLEXI_75K_2; 1.
TE; PS00643; COMPLEXI_75K_3; 1.
                                                                                                                                                                                                                                                                                                                          853 AA
              12.9%; Score 72.5; D 29.0%; Pred. No. 11; ive 14; Mismatches
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Interpro; IPR000283; Complex1_75K.
Interpro; IPR0010041; Ferredoxin.
Pfam: PF00037; fer4; 1.
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PF00384; molybdopterin; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pSymA (megaplasmid 1).
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                   Best_Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                      NUG2_RHIME
P56914;
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PROSITE;
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekela F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J., St., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
Laborovool (Rel. 41, Last annotation update)
Putative flavin-containing monoamine oxidase Rv3170 (EC 1.4.3.-).
Rv3170 OR MT3259 OR MTV014.14.
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-!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                              POTENTIAL)
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F -> L (IN REF. 1).
T -> I (IN REF. 1).
T -> I (IN REF. 1).
S -> G (IN REF. 1).
R -> K (IN REF. 1).
R -> C (IN REF. 1).
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                        IRON-SULFUR (IRON-SULFUR (IRON-SULFUR (
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IRON-SULFUR
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STRAIN-CDC 1551 / Oshkosh;
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                        laboratory strains.";
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les 16; Conser'
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053320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parker N.J., Begley C.G., Smith P.J., Fox R.M.;
"Molecular cloning of a novel human gene (D11S4896E) at chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOSYLATION, PHOSPHORYLATION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manji S.S., Parker N.J., Williams R.T., van Stekelenburg L., Pearson R.B., Dziadek M., Smith P.J.; "STIMI: a novel phosphoprotein located at the cell surface."; Biochim. Biophys. Acta 1481:147-155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21356314; PubMed-11463338; Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S., Wan Stekelenburg L., Eid J.-P., Senior P.V., Kazenwadel J.S., Shandala T., Saint R., Smith P.J., Dziadek M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 65.5; DB 1; Length 454; 31.5%; Pred. No. 15; Live 12; Mismatches 27; Indels II:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00757; AMINEOXDASEF.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAD (ADP PART) (POTENTIAL). 6C1AEB97FB2F435F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
STIM1 OR GOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculist, Rv3170; ...
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001613; Amineoxid_f1.
                                                                                                                                                                                                                                                                      EMBL; AL021646; CAA16635.1; ALT_INIT.
EMBL; AE007139; AAK47598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20461006; PubMed=11004585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Placenta, and Fetal liver; MEDLINE-97079692; PubMed-8921403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY, AND SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 37:253-256(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 31.5
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                            P27338; 1GOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 AA;
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                                                                                                                                                                                                                                                                                                                                                                           TIGR; MT3259; -
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                              FUNCTION: Possible adhesion molecule with a role in early hematopoiesis by mediating attachment to stromal cells. Influences the survival and/or proliferation of B cell precursors. Binding to cells requires Mn(II) (By similarity).
SUBGELLUIAR LOCATION: Type I membrane protein. Cell surface
                                                                                                                                                                                                                                                          MEDLINE-98021968; PubMed-9377559; Sabbionis, Negrini M.; Sabbioni S., Barbanti-Brodano G., Croce C.M., Negrini M.; GOK: a gene at 11p15 involved in rhabdomyosarcoma and rhabdoid tumor development.";
"Identification and characterization of the STIM (stromal interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 EETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTNSAMRA---- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMARY; SM00454; SAM; 1.

PROSITE; PS50105; SAM_DOMAIN; 1.

Cell adheaion; Anti-oncogene; Transmembrane; Coiled coil; Signal; Glycoprotein; Phosphorylation.
SIGNAL 1 22 STROMAL INTERACTION MOLECULE 1.

CHAIN 23 685 STROMAL INTERACTION MOLECULE 1.
         molecule) gene family: coding for a novel class of transmembrane proteins.";
                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Ubiquitously expressed in various human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches 38; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STROMAL INTERACTION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 --GHLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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Pred. No. 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAM
                                                                                                                                     57:4493-4497(1997).
                                      Biochem. J. 357:673-685(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77492 MW;
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InterPro; IPR001660; SAM.
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CAML_MOUSE
ID CAML_MOUSE
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TISSUE-Brain:

**REDLINE-8818924; PubMed=3412448;

**MEDLINE-8818924; PubMed=3412448;

**MEDLINE-8818924; PubMed=3412448;

**MEDLINE-8818924; PubMed=3412448;

**MEDLINE-8818924; PubMed=341248;

**MEDLINE-8818924; PubMed=341248;

**Incharal adhesion molecule L1 as a member of the immunoglobulin superfamily with binding domains similar to fibronectin.";

**Incharal adhesion molecule L1 as a member of the immunoglobulin substance of the immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
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InterPro: 1PR003961; FNLII.
InterPro: 1PR003962; FNLII.
InterPro: 1PR003962; FNLII.
InterPro: 1PR003969; FNLII.
InterPro: 1PR003006; Ig_MHC.
InterPro: 1PR003006; Ig_LHC.
InterPro: 1PR003006; Ig_Like.
InterPro: 1PR003006; Ig_Like; I.
SMART; SM00410; IG_Like; I.
SMART; SM00408; IGC2: 5.
IGUIL adhesion; Glycoprotein; Transmembrane; Repeat; Brain; Immunoglobulin domain; Signal.
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POTENTIAL.
CYTOPLASHIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 6.
FIRROMECTIN TYPE-III 1.
FIBROMECTIN TYPE-III 3.
FIBROMECTIN TYPE-III 3.
               01-077-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neural cell adhesion molecule L1 precursor (N-CAM L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X12875; CAA31368.1; -.
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HSSP; P20241; 1CFB.
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Pred. No. 47;
        N-LINKED GECNAC.
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Job time : 7.1707 secs
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27.98;
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Matches 19; Conservative
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Q9cda mycobectri

Q9cap8 drosophila

Q9rcp8 drosophila

Q9rag drosophila

Q9rag thermoplasm

Q9al8 clostridium

Q9al8 clostridium

Q9al8 clostridium

Q9al8 clostridium

Q9al10 potato viru

Q9lht2 potato viru

Q91555 potato viru

Q9657 potato viru

Q9673 mus musculu

Q9673 mus musculu

Q9671 prococcus
                                                                                                                                                                                                              09w1q6 drosophila
09s434 myxococcus
069441 legionella
030119 archaeoglob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 EEDALWENVECNRHMLSRYINPAKLTPYLRQCKVIDEQDEDEVLNAPMLPSKINRAGRLL 94
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 48.2%; Score 270; DB 4; Length 1171; Local Similarity 51.5%; Pred. No. 2.9e-22; es 51; Conservative 22; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLJ00120 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1171 AA
                                                                                                                                                                                                                                                                  ALIGNMENTS
        099NA19
099TUD6
099TUD6
099NCP8
099NCP8
099NCP8
091R29
091R29
091R78
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=SPLEEN;
NCBI_TaxID=9606
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Q66677 equine herp
Q97el5 clostridium
Q9yjn5 equine herp
O61218 caenorhabdi
Q9v466 drosophila
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Q8tdn1 homo sapien
Q9ddu9 xenopus lae
Q9p3s8 neurospora
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Q95zc3 leishmania
Q9btq5 homo sapien
Q96h24 homo sapien
Q96et5 homo sapien
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                                                                 (without alignments)
1321.544 Million cell updates/sec
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                                                       January 22, 2003, 08:49:36; Search time 16.6828 Seconds
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1 ALTALDEETLWEMMESHRHR......PDVYTLVTGLQPDVDFSNFS 107
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       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                   671580 segs, 206047115 residues
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                                        - protein search, using sw model
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Q99PQ2
Q69PQ2
Q9YZUS
Q9YZUS
O61218
Q9YZD1
Q9WZD1
Q9SZC3
Q9EZC3
Q9ERQ5
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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sp_virus:*
sp_vertebrate:*
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sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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seq length: 200000000
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EMBL; U20824; AAC13865.1;
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                                                                                                     SEQUENCE
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Q97EL5;
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Q9YJN5
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                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-21231161; PubMed-11331580;

Reymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,

Riganelli D., Zanaria E., Messali S., Calnarca S., Guffanti A.,

Minucci S., Pelicci P.G., Ballabio A.;

"The tripartite motif family identifies cell compartments.";

EMBO J. 20:2140-2131(2001).

EMBL: AF220124; AAG53497.1;

HSSP; P15919; 1RMD.

MGD; MGI:2137355; Trim11.
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MEDILINE-95302501; PubMed=7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
"The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 467;
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA; 52579 MW; 82B7CF68807E9DA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus type 2 (strain 86/87) (EHV-2). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae.
                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 75; DB 1
32.2%; Pred. No. 3.4;
467 AA
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    PRT;
                                                                                                         Tripartite motif protein TRIM11.
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    PRELIMINARY;
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                                                                                                                                                Mus musculus (Mouse)
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SEQUENCE FROM N.A.

MEDLINE=21359325, PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubods J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Glostridium accobutylicum.";
J. Bacteriol. 183:4823-4838 (2001).

EMBL; AE07806; AR81035-1;
InterPro; IPR004399; HMP-P.Kinase.
TIGRPAMS; TIGR00097; HMP-P.Kinase; I.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                            ----MESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVL 49
                                                                                                                                                                                                                                                                                                                                                                            16 LTEEDIWDVERLCLEELRVLLVSHLKSHKH------LDHLRAKKILSREDAEEV- 63
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                                                                                                                                                                                   13.0%; Score 73; DB 12; Length 210; 29.5%; Pred. No. 2.3; ive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase; Complete proteome.
SEQUENCE 265 AA; 28539 MW; 327DA3CEAE6D06EB CRC64;
                                                                                                                         22943 MW; 136D639DD8BC2D40 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 32.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Hydroxyethylthiazole kinase ThiM/ThiK (FS!).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 AA
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InterPro; IPR001315; CARD. Pfam; PF00619; CARD; 1. SMART; SM00114; CARD; 1. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                      Query Match 13.0%
Best Local Similarity 29.5%
Matches 28; Conservative
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                 Thome M., Martinon F., Hofmann K., Rubio V., Steiner V., Schneider P., Mattman C., Tschopp J.;
Rguine herpesvirus-2 E10, but not its cellular homologue, activates NF *B transcription factor and c-jun N-terminal kinase.";
J. Biol. Chem. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Filton L., Gardher A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Bukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                   Willis T.G., Jadayel D.M., Du M.Q., Peng H., Perry A.R.,
Abdul-Rauf M., Price H., Karran L., Majekodunmi O., Wlodarska I.,
Apan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.;
"Bcll0 is involved in t(1;14)(p22;q32) of MALT B cell lymphoma and
mutated in multiple tumor types.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 311 AA; 32602 MW; 04EC68C7353D723B CRC64;
  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and apoptosis.";
J. Biol. Chem. 274:17946-17954(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                    MEDLINE=99142601; PubMed=9989495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE-94150718; Pubmed-7906398;
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EMBL; AF100340; AAD16430.1; -.
EMBL; AF134394; AAD39146.1; -.
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29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001315; CARD.
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PROSITE; PS50209; CARD; 1.
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                                                                               SEQUENCE FROM N.A.
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                                      NCBI_TaxID=133899;
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Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Botshakov S.,
A. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis S.,
A. de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonhhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 71; DB 5; Length 265; 23.9%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ------AGHLL----DLLKTRGKNGAIAFLESLKFHNPDVYTLVTG 96
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                                                                                                                                                                                                                                                                                                                                                                                                          cosmid K03H6.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF047658; AAC04418.1; -.
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PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SEQUENCE 265 AA; 30644 MW; E7536832B08BDAFA CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000734; Lipse.
InterPro; IPR002921; Lipase_3.
InterPro; IPR000834; Zn_carbopept.
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                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of C. elegans
Submitted (FEB-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.9%;
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BCDNA:LD18761 OR CG6743.
                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                           STRAIN=BRISTOL N2;
Wamsley P., Gibson A.;
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095ZC3
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Matches
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Q952C3
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Racsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Garell J.H., Gu Z., Guan P., Harris M., Ratush R., Harvey D., Helman T.J., Hernandez J.R., Ibeuck J., Ra Harris D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Radiali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Ratush B.E., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Liang Y., Lin X., Ratushov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA, Mount S.M., Melson R.N., Nelson D.L., RA Palazzolo W., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Spier E., Standing A.C., Standers R.D. C., Scheeler F., Shen H., RA Spier E., Standing A.C., Standers R.D. C., Stone B.C., Standers R.D. C., Stone B.C., Stand M., Strong R., Sun E., Sand M., Marshy D., Weissenbach J., Mang Z.-Y., Hassarman D.A., Weinstock G.M., Weissenbach J., Wang S., Yao, Yao, Zaveri J.S., Zaveri J.S., Zhan M., Zhang G., Zhang C., Zheng L., The genome sequence of Drosophila melanogaster.";
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MEDLINE-95287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LTALDEETLWE----MMESHR-----HRIVRCICPSRLTP--YLRQAKVLCQLDEEEV 48
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 70.5; DB 5; Length 845; 30.7%; Pred. No. 22; Live 13; Mismatches 36; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                    Tsang G., Brokstein P., Frise E., Harvey D., Evans-Holm M., Lewis S.E., Suh C., Rubin G.M.;
"Full Length Drosophila melanogaster cDNA sequence.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003629; AAF33002.1;
EMBL; AF160938; AAD46878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 845 AA; 97381 MW; 0A75B807A6AFD6B6 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein TM0663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0027868; BcDNA:LD18761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
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Best Local Similarity
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Q9WZD1;
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                   8 ETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLTN----SAMRAG 62
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                                                                                                                                                        Gaps
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NCBI_TaxID=5664;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                        21;
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MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                Length 522;
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EMBL; ALS96274; CAC44741.1; -.
SEQUENCE 979 AA; 102709 MW; D43039D7F172DE02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 979;
                                                                                                                                                                                                                                                                                                                             407 YWDFPHILD-LDERVLNGAV-YIHS----TSEAYT----EEQEIDAKRF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Rieger Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
EMBL; AE001739; AAD35747.1; -.
TIGR; TM0663; -.
Hypothetical protein; Complete proteome.
SEQUENCE 522 AA; 60668 MW; D7A5E16AA88F79CC CRC64;
                                                                                                                                                                                                                                                                                              63 ----HLLDLLKTRGKNGAIAFLESLKFHNPDVYTLVTGLQPDVDFSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 24.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Possible hypothetical 110.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                             12.4%; Score 69.5; DB 16; 28.4%; Pred. No. 17;
                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 KVLCQLDEEEV-LHSPRL---TNSAMRAGHLLDLLKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           979 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 69; DB 34.8%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 PAFAFLGE-KFNHPCMLYYRWRLYSLLQG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GAIAFLESLKFHNP-----DVYTLVTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L1994.04
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TISSUE=OVARY;
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8VDX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VDX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
Q8TDN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VDX5
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
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                                                                                                                                                                                                                                                                                                                                                                                            1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLT----N 56
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown (protein for MGC:4558).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    096ET5.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 28.4 kDa protein.
Homo sapical Actazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                              6 DEE--TLWEMMESHRHRIVRCICPSRLTPYLRQAKV-----LCQLDEEEVLHSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 SAMRAGHLLDLLKTRGKN-----GAIAFLESLKFHNPDVYTLVTGLQPDV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.1%; Score 68; DB 4; Length 256; Best Local Similarity 25.2%; Pred. No. 11; Matches 28; Conservative 20; Mismatches 49; Indels
                                                                                                                                                                                                                                                                 Query Match 12.1%; Score 68; DB 4; Length 221; Best Local Similarity 28.7%; Pred. No. 9.2; Matches 29; Conservative 11; Mismatches 45; Indels
                                          Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BE003520; AAH03520.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                SMARY; SM00320; WD40; 1.
Hypothetical protein; Repeat; WD repeat.
SEQUENCE 221 AA; 24472 MW; 39CCF8979C10DB53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .ra; 1.
29333 MW; 5A48EFC68637F8B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096H34;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 IRLLGFDKQCSELVDCLPKEA--SPLRVIRSLYSHNDVVLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 -RLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAY-2001) to the EMBI EMBL; BC008969; AAH08969.1; -.
Interpro; IPR003131; K_tetra.
Pfam; PF02214; K_tetra; 1.
SEQUENCE 256 AA; 29333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A. TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96ET5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                          160 EETCALWQKMVESQRQNVLGEF--ERLRRLLAEEEQQLLQKLEEEELEVLPRLREGAARL 217
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                         6 DEE--TLWEMMESHRHRIVRCICPSRLTPYLRQAKV-----LCQLDEEEVLHSP---- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 EET--LWE-MMESHRHRIVRCICPSRLTPYL--RQAKVLCQLDEEEVLHSPRLTNSAMRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_maxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Learning R.;

Lauring R.;

Loudited (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC020102; AAH20102.1;

R InterPro; IPR001870; Gamma_carbxylse.

R InterPro; IPR001870; Gamma_carbxylse.

R InterPro; IPR001870; SPRY_domain.

R InterPro; IPR001841; Znf_lbox.

R InterPro; IPR001841; Znf_lbox.

R Pfam; PF00062; SPRY; 1.

R Pfam; PF000643; Zf-Bbox; 1.

R Pfam; PF000643; Zf-Bbox; 1.

R Pfam; PR001841; Zf-C3H44; 1.

R Pfam; PR001841; RICS.HOSEN.

SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 483;
23;
                                                                                                                                                                                                                                         Length 258;
                                                                                                                                                                                                                                                                                         45; Indels
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: CONTAINS 1 WD REPEAT (TRP-ASP DOMAIN).
EMBL; BC011959; AAH11959.1;
EMBL; BC011959; AAH11959.1;
EMBL; PF00400; RP040; 1.
Hypothetical protein; Repeat; WD repeat.
                                                                                                                                                           11 protein; Repeat; WD repeat.
258 Aa; 28385 MW; F50D287B1FAEE9E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS5018; ZF_RING_1; UNKNOWN_1.
PROSITE; PS50089; ZF_RING_2; 1.
SEQUENCE 483 AA, 54313 MW; 51BDFFCD514046FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to tripartite motif protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 IRLLGFDKOCSELVDCLPKEA--SPLRVIRSLYSHNDVVLT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                               53 -RLTNSAMRAGHLLDLLKTRGKNGAIAFLESLKFHNPDVYT 92
                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 AA
                                                                                                                                                                                                                                 12.1%; Score 68; DB 28.7%; Pred. No. 11; ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 68; 32.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                              Best_Local Similarity 28.7%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE—20570484; PubMed=11114187;

MEDLINE—20570484; PubMed=11114187;

MIDLINE—20570484; PubMed=11114187;

Tidentification of XPR-1, a progesterone receptor required for Xenopus ocyte activation.";

TOC: Natl. Acad. Sci. U.S.A. 97:1438-14363(2000).

TOC: Natl. Acad. Sci. U.S.A. 97:1458-14363(2000).

TOC: Natl. Acad. Sci. U.S.A. 97:1480.

TOC: Natl. Acad. Sci. U.S.A. 97:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 ALSFQEELAYWGIEEAH---LERC-CLRKLLRKLEELEELAKLHREDVLRQQRETRRPAS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALTALDEETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPRLT----N 56
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Oltschytzsch N., van Hoorick D., Raes A.L., Snyders D.J.;

Oltschytzsch N., van Hoorick D., Raes A.L., Snyders D.J.;

Channel subunits.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR548984; AAL83911.1;

Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0047; STROIDFINGER.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR000047; STROIDFINGER.
SMART; SM00430; Lac. C4steroid; 1.
SMART; SM00399; ZnF_C4; 1.
SMART; SM00399; ZnF_C4; 1.
DNA-binding; Nuclear_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 HSSRWGLCMNRLREMVENPQSGLPGKVFACLSILFVATTAVSLCVSTMPDL 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 68; DB 4; Length 519; 25.2%; Pred. No. 25; tive 20; Mismatches 49; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Voltage-gated potassium channel KV6.3.
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Pfam; PF00105; zf-C4; 1.
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Matches 28; Conservative
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XPR-1.
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NCBI_TaxID=8355;
                                                                                                                                          Homo sapiens (Human).
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Search completed: January 22, 2003, 08:56:31 Job time : 20.6828 secs

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January 22, 2003, 08:49:35; Search time 57.4933 Seconds (without alignments) 683.714 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Human caspase recr	Human predicted ca	Human caspase recr	Human caspase recr	Human plakoglobin	Rat caspase recrui	Human caspase recr	Human polypeptide,	Human protein sequ	Novel human diagno
SUMMARIES		ID		AAE07164	AAE07165	AAU01207	AAU01206	AAU73247	AAU01204	AAU01205	AAM93822	AAB95617	ABG05850
		DB	1	22	22	22	22	23	22	22	22	22	22
		Query Match Length DB		1004	1139	1147	1032	1032	536	536	746	366	2246
	æ	Query Match		100.0	98.7	27.1	22.5	22.5	19.4	18.8	15.7	13.5	13.5
		Score	1 1 1 1 1 1 1	1462	1443	396.5	329.5	329.5	283.5	274.5	230	198	197
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AAB95546 AAR47173 AAG5579 AAU32041 AAU32041 AAW41931 AAW41931 AAW41937 ABB58673 AAW40937 AAW4083 AAW4083 AAW4083 AAW4083 AAW40372 AAW40372 AAW40372 AAW40373 AAW40373 AAW40373 AAW40373 AAW40372 AAW40373	ain-14 (C main-14; cell gr coll gr odysplast n's disea odysplast n's disea ofysplast o
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(MILL-) MILLENNIUM PHARM INC.
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760..763
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N-PSDB; AAD13447.
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                                                                                                  Domain
700.472
/note= "Protein kinase C phosphorylation site"
501..504
/note= "Casein kinase II phosphorylation site"
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253. 256
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366..368
/hote= "Protein kinase C phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
378.381
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.e= "Casein kinase II phosphorylation site"
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297..300
/note= "Casein Kinase II phosphorylation site"
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Note= "Casein kinase II phosphorylation site"
159.365
Note= "Tyrosine kinase phosphorylation site"
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384..386
/note= "Protein kinase C phosphorylation site"
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163..466
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.e= "Casein kinase II phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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  60..62
/note= "Protein kinase C phosphorylation site"
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te= "Tyrosine kinase phosphorylation site"
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note= "Leucine zipper pattern"
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/note= "N-myristoylation site"
589..592
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.e= "N-myristoylation site"
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'note= "N-myristoylation site"
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note= "cAMP- and cGMP-dependent protein kinase hosphorylation site" site" 941..949
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740.947
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368..870
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                                                                                 The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimulates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders e.g., haematological disorders (e.g., anaemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infactions.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                                                                                                                                      ; Score 1462; DB 22;
; Pred. No. 6.9e-107;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers Misc-difference 700
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                                                    Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07165 standard; Protein; 1139
                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                      1004 AA;
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
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(CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., annume disorders (e.g., crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
                                                                                                                                                                    An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                      present sequence is predicted human caspase recruitment domain-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1443; DB 22;
Pred. No. 2.6e-105;
0; Mismatches 0;
                                                                                                                                                                                                                           Disclosure; Fig 2A-2C; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01207 standard; Protein; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.7%;
94.2%;
                                                                    (MILL-) MILLENNIUM PHARM INC
             22-JAN-2001; 2001WO-US02087.
                                        09-FEB-2000; 2000US-0181159.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.2
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
                                                                                                                           WPI; 2001-497073/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEPPGVLKQEART
                                                                                                                                        N-PSDB; AAD13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2001
                                                                                                Bertin J;
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             Jomain
apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "cAMP- and cGMP-dependent protein kinase
  phosphorylation site"
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phosphorylation site"
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508..510
/note= "Protein kinase C phosphorylation site"
510..513
                                                                                                                                                                                                                                                                                                                                          130..431
/note= "Coiled coil domain"
162..165
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290..292
Anote= "Protein kinase C phosphorylation site"
78..381
129..432
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/note= "protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Protein kinase C phosphorylation site" 78..581
note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'notes" Amidation site"
86. 289
'notes" Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                              168..171
//note= Casein kinase II phosphorylation site" //note= Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443..245
/note= "Protein kinase C phosphorylation site"
282..285
                                                                                                                                                                                                 102
e- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                . 103
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                "Protein kinase C phosphorylation site"
                                                                                                                                               'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                            75..183
note- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..195
te- "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "cAMP- and cGMP-dependent protein
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-myristoylation site"
34..637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72..475
"note= "N-glycosylation site"
76..479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...244
ote= "N-glycosylation site"
                                                                                                                 'note≕ "CARD domain"
                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Ci
584..587
/note= "N
587..592
                                                                                                                                                                                                                                                                                               .109
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                                                   Homo sapiens
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/note= "N-myristoylation site"
1088.1091
/note= "Casein kinase II phosphorylation site"
1120.1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Casein kinase II phosphorylation site"
/note= "Casein kinase II phosphorylation site"
882..1147
/note= "Guanylate kinase (GUK) domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .900
e= "Casein kinase II phosphorylation site"
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:e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                       note= "N-glycosymucc...
79.782
'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                 .789
.e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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ce= "Protein kinase C phosphorylation site"
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                                                                                                        687..689
/note= "Protein kinase C phosphorylation site"
692..695
                                                                                                                                                                                                        10.00ce "N-myristoylation site"
25..728
note= "casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Tyrosine kinase phosphorylation site" (050..1055
                                                            "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                               note= "Protein kinase C phosphorylation 003..1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                      /no.e.
/note= "SH3 domain"
/76.779
/note= "N-glycosylation site"
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153..858
//orte= "N-myristoylation site"
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.e= "N-myristoylation site"
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te- "N-myristoylation site"
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te= "N-myristoylation site"
                                                                                         "N-myristoylation site"
                                 "MAGUK domain"
/note= "PDZ domain"
635..1147
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18-FEB-2000; 2000US-0507533.
25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
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335..937
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CARD-10;

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/note= "N-glycosylation site"
  Human; caspase recruitment domain;
                                                                                     Key
Modified-site
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 The present sequence represents novel numan caspase recruitment domain, CARD-11. The polyvuclectide encoding this sequence was isolated from a human T-cell cDNA library, Also described are covel human sequences for CARD-9 and CARD-10 (AAU01205). AAU01206)

and rat CARD-9 (AAU01204). CARD-9, CARD-11 interact and appotosis: The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by creating the expression or activity of CARD-9, CARD-10, or CARD-11. CR They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (c.g. cancer), advisorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (c.g. cancer), advisorders (e.g. disease), inflammatory disorders (c.g. cancer) and viral infection (e.g. HTV). The CARD can be used in screening and detection assays (e.g. chromosomal campping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or cancer, modulate it. CARD sequences are potential targets for regulating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host call containing a polynucleotide capprocess are potential armagenic animals.
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9
                                                                                               Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMNEVIKLQQQMKAKDLQRCELLARLRQLEDEKKQMTLTRVE-LLTFQERYYKMKEERDS 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNDELVKVKDDNYNLAMRYAQLSEEKNMAVMRSRDLQLEIDQLKHRLNK--MEEECKLE-
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RNQSLKLKNDIENRPKKEQVLELERENEMLKTKNQELQSIIQAGKRSLPDSDKAILDILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDRKEALEDRQELVNRIYNLQEEARQAEELRDKYLEEKEDLELKCSTLGKDCEMYKHRMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                     present sequence represents novel human caspase recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.1%; Score 396.5; DB 22; 34.0%; Pred. No. 1.1e-22; ive 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEQSLRTASDQES - - GDEELNRLKEENEKLRSLTFSL -
                                                                                                                                                       Claim 9; Fig 14A-14C; 145pp; English.
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Matches 102; Conservative
                                                                                                                             and detection assays
                                                       2001-367809/38
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apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570..573
/note= "Casein kinase II phosphorylation site"
595..598
                                                                                                                                                 'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                              note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...295
Le= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                      .115
.e= "Casein kinase II phosphorylation site"
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'note= "Protein kinase C phosphorylation site"
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Bcl-10; NF-kappaB;
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.e= "Tyrosine kinase phosphorylation site"
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ce= "Casein kinase II phosphorylation
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e- "Casein kinase II phosphorylation
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te= "Protein kinase C phosphorylation
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                                                                                                                                                                                                                                                                        'note= "Protein kinase C phosphorylation
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/note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                        'note= "Amidation site"
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/note= "CARD domain"
58..70
                                                                                       Location/Qualifiers
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/note= "Casein Kindow -- .
754..756
/note= "Protein Kinase C phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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1028..1031
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/note= "Casein kinase II phosphorylation site"
603..605
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                            ..751
te= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
                                      .644
.e= "Protein kinase C phosphorylation site"
                                                                                                          "Casein kinase II phosphorylation site"
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                                                                                                                                                                  "Casein kinase II phosphorylation site"
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te= "Tyrosine kinase phosphorylation site"
         /note= "Proteru name."
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                                                                                                                                                                                                                                                                                                                                                                                          .885
.e= "Casein kinase II phosphorylation
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/note= "Guanylate kinase (GUK) domain"
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1021..1026
note= "N-myristoylation site"
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                                                       ..661
te= "N-myristoylation site"
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                                                                                                                  704..772
/note= "SH3 domain"
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714..717
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25-FEB-2000;
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The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated domain, CARD-10. The polynucleotide encoding this sequence was isolated from a human skin CDNA library. Also described are novel human sequences for from a human skin CDNA-11 (AAU01205, AAU01207) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappab and apoptosis. The sequences of the invention can be used for treating a disorder sescited with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. CARD-10, or CARD-11. They can be used for the treatment of sorders (e.g. cancer), autoimmune disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), concreen for drugs that bind to and/or modulate it. CARD sequences are potential targets for requilating inflammation, cancer, NF-kappab signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
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9
                                       Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 LMTEVRRLREARKSQLQREQQLQARGRVLEEERAGLEQRLRDQQQAQERCQRLREDWEAG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQSLRTASDQESGDEELNRLKEENE------KLRS----LTFSLAE----- 158
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Pred. No. 1.8e-17;
0; Mismatches 115; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human plakoglobin interacting protein #3.
                                                                                                                                 Claim 9; Fig 10A-10C; 145pp; English.
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31.8%;
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N-PSDB; AAS05388
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases, include basal cell carcinoma, extranammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/skin fragility syndrome. AAU73245-AAU7324 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of
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plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; Maxos disease; extramammary Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darler's disease; skin fragility syndrome.
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AERDELLTTLTSLE 441
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N-PSDB; AAS98203.
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Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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te= "Casein kinase II phosphorylation site"
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/hote= "Coiled coil domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents novel rat caspase recruitment domain, CARD-9. The polynuclectide encoding this sequence was isolated from a rat neuronal cDNA library. Also described are novel human sequences for CARD-10 and CARD-11 (AAU01205).

CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-Kappas and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression of the invention can be used for treatment of hyperproliferative disorders (e.g. cractivity of CARD-19, CARD-10, or CARD-11. They can be used for activity of CARD-9, CARD-10, or CARD-11. They can be used for autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. planier's disease), and wiral infection (e.g. HIV). The CARD polypeptide, polynuclectide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQ-SLRTASDQESGDEELNRLKEENE----KLRSLTFSLAEK------DILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences are potential targets for regulating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
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ce- "Protein kinase C phosphorylation site"
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Matches 91; Conserv
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                                                                                     169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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e= "Protein kinase C phosphorylation site"
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7..98
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197..213
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Mismatches Pred. No.

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Conservative

28.48;

Similarity

Local Sim-87;

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ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ

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FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122 172 SRELKRCKEENYDLAMRLAHQSEEKGAALMRNRDLQLEIDQLKHSLMKAE--DDCKVERK 229 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168 || | :| | :| | :| | ::| | | : | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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ESGLTQLLMTEVWKLQKKVQDLTALLSSKDDFIKELRVKDSLLRKHQERVQRLKEECEAG 171

EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS---

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The presult sequence represents movel immunicated was isolated from a human megakaryocyte cDNA library. Also described are novel human sequence for CARD-10 and CARD-11 (AAU01207) and rat CARD-9 sequences for CARD-10 and CARD-11 interact with Bcl-10 which is sequences for CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can cerv. activity of CARD-9, CARD-10, or CARD-11. They can cerv. activity of CARD-9, CARD-10, or CARD-11. They can cerv. activity of CARD-9, CARD-10, or CARD-11. They can cerv. activity of CARD-9, CARD-10, or CARD-11. They can cerv. activity of CARD-10, are activity of CARD-10, and the disease, infinamatory disorders (e.g. Alzhelmer's disease), infinamatory disorders (e.g. Alzhelmer's disease), infinamatory disorders (e.g. CARD can be used in screening and detection assays (e.g. chromosomal mapping), tissue typing), predictive medicine (prognostic assays).

CARD polypeptide may be used to screen for drugs that bind to and/or monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD sequences are potential targets for regulating and inflammation, cancer, MorkappaB signalling, stress-related response and appetosis in human disease. A host call containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
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 .428
e= "Casein kinase II phosphorylation site"
                               ..433
Le- "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
                                                                                       "Protein kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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e- "N-myristoylation site"
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25-FEB-2000; 2000US-0513904.
10-OCT-2000; 2000US-0685791.
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N-PSDB; AAS05387.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their
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S, Otsuki T, Koga
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                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping.
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K, Kojima S
                                                                                             AAM93822 standard; Protein; 746 AA.
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a T, Nagai
                                                                                                                                                                              SEQ ID NO:
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11-JAN-2000; 2000JP-0118774.
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N-PSDB; AAK94778.
                                                                                                                                                                               Human polypeptide,
LKQEAR 294
                         LAVEGR 412
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Length 536;

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18.8%; Score 274.5;

Query Match

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without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                   :: : ||: |::|||||| :|| | : ||||| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|
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Otsuki
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                                                                                                                                                             15.7%; Score 230; DB 22;
41.5%; Pred. No. 8.8e-10;
iive 25; Mismatches 47
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A, Nagai K,
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T, Wakamatsu A,
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99JP-0300253.
2000JP-0118776.
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2000JP-0241899
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les 51; Conservative
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09-JUN-2000;
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11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   280 QLQ 282
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polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as illy without any specialised methods. AAH03166 to AAH13628 and AAH13613 to AAH13612 to AAH13612 end and coid sequences; and AAH13612 to AAH13612 represent human anino acid sequences; and AAH13612 to AAH13612 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 HTLKLRHAMEQRPSQELIMELQQEKALLQARVQELEASVQEGKLDRSSPYIQVLEEDWRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                          of the present invention
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   366 AA;
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28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                     polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010 ABG30377 represent novel human amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: |: || || || || :| || 1013 KEKQAQLAQTLQQQEQASQXLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-Q 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AHFHEVLRLKDEMLSLS------1HYSNALQEKELAASRCRSLQEELYL---- 103
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894 GDVLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLIT
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Mismatches 108; Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2246;
                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
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                                                                                                       Claim 20; SEQ ID No 36209; 103pp; English
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. The complementary to a polynucleotide which comprises a 3'-end sequence, and an oligonucleotide comprises at 3'-end sequence, where the oligonucleotide which comprises as 1'-end sequence, where the oligonucleotide comprises at 15 nucleotides and the combination of the 5'-end sequence, and sequence; selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers also useful for the full-length cDNAs. The primers also useful for the full-length cDNAs. The primers also useful for AMH13628 and AMH13613 to AMH13613 to AMH13631 Lepresent human amino acid sequences; and AMH13629 to AMH13632 represent human amino acid sequences; and AMH13632 to AMH13632 represent human amino acid sequences; and AMH13632 to AMH13632 represent human amino acid sequences; and AMH13632 to AMH13632 represent human amino acid sequences; and AMH13632 to AMH13632 companion and AMH13632 and AMH13633 companion and AMH13632 and AMH13633 companion and AMH13633 companion amino acid sequences; and AMH13632 to AMH13632 companion and AMH13632 companion and AMH13632 companion and AMH13633 compani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ-EQSLRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: :: : : : : | | : | | : | | : | | : | : | : | : | : | EBALVHV -----RKEEKAVSAR-RALENEL-----EAAQGNLSQTTQEQKQLSEKLKE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 ASDQESGDEELNRLKEENEKLRSLTFSLAEK-----DILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESEQK---EQLRRLKNEMENERWHLGKTIEKLQKEMADIVEAS----RTSTLELQNQLDE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LRE--RAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69
                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
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                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SARDSAQREISQSLVE-----KDSLRRQVFELTDQVCELRTQLRQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 196; DB 22; 25.8%; Pred. No. 3.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 18167; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                          Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                            99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
    99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
                                                                                         11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                             09-JUN-2000;
29-JUL-1999;
                                                 27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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----TDQVCELRTQLRQLQ 282

qq

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531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                      187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                 | ::|: || || || || || 635 QISVIQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                  QREISQSLVEKDSLRRQVFEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bissell M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-610603/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Number Z11584).
                                                                                                                                                                                                                                                                                                                                                                                                                              US6287790-B1.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1998;
                                                                                                                                                                                                                                                                                30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lelievre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                AAG65799;
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                                                                                                  247
                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                  AAG65799
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                                 οy
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                                                                                                   ΩŊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIT and MT2 proteins were islated from malignant cells essentially following the method of Penman and Fey, described in US Pat. Nos. 4, 882,286 and 4,885,236. DNA sequences encoding these proteins were cloned by probing expression libraries using monoclonal antibodies raised against the isolated INM proteins. The genetic sequence encoding MT2 has been disclosed by Yang et al. 1992, J. Cell Biol. 116:1395-1408, and is referred to by them as 'NuMA'. The nucleotide sequence encoding MT1 has not beed described previously. Both the MT1 and MT2 proteins are distributed throughout the nucleus (with the expinole during mitosis. A binding protein having a binding affinity of greater than about 10(9) M(-1) for AAR47173 is claimed for use in the manufacture of a medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NEKLRSLIFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412 VLOLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 -----AKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel malignant cell type markers of the interior nuclear matrix - used for detecting abnormal cell types e.g. malignant breast, prostate, lung, etc., for determining deg. of cell death in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL----
                                                                                                                                                                                                                   Malignant cell type marker; interior nuclear matrix; MT2; NuMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
      343 TKRQLLEQTLKDLEYELEAKSHLKDDRSRLVKQMEDKVSQLEMELEE 389
                                                                                                                                                                                    the inner nuclear matrix (INM) protein MT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3%; Score 194; DB 15; Best Local Similarity 26.6%; Pred. No. 2.2e-06; Matches 93; Conservative 49; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 56-66; 93pp; English.
                                                                                       AA.
                                                                                      AAR47173 standard; Protein; 2101
                                                                                                                                                                                                                                                                                                                                                  93WO-US06160.
                                                                                                                                                                                                                                                                                                                                                                                  92US-0901701
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Toukatly G;
                                                                                                                                                                                                                                                                                                                                                                                                                  (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-026210/03.
N-PSDB; AAQ54841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2101 AA;
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  21-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lidgard GP,
                                                                                                                                                      15-JUL-1994
                                                                                                                                                                                      Sequence of
                                                                                                                                                                                                                                                                                   WO9400573-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue, etc.
                                                                                                                                                                                                                                                                                                                   06-JAN-1994
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                                                                                                                    AAR47173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                           RESULT 12
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                                                                                                                                                                                                                                                                                   NuMA; Nuclear Mitotic Apparatus protein; malignant; cell growth; human;
tumor progression; structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distinguishing growth arrested malignant cells from proliferating non-malignant cells, comprises staining the nuclear mitotic apparatus protein in intact mammalian cells and determining the 3-dimensional pattern of the labeled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LHYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2101;
                                                                                                                                                                                                               Nuclear mitotic apparatus protein (NuMA) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 104;
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Pred. No. 2.2e-06;
   Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 15; 38pp; English.
AAG65799 standard; protein; 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0452294.
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New nucleic acid encoding nuclear mitotic appts. interacting
2117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW21732;
  Sequence
                        Query Match
                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                Matches
                                                                                                                                             412
                                                                                                                                                                     104
                                                                                                                                                                                                                     146
                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                             AAW21732
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                                                                                             Dp
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                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to increase stem cell proliferation, to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                    -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                       AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
412 VLOLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
                                                                      --NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                           586 ATAAE-EREASLRERDAALKOLE-----ALEKEKAAKLEI----LOOOLOVANEARDSA 634
                                                                                                                                                                                                                                                                                                                                                    Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                ------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                        635 QTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                                                                                        AAU32040 standard; Protein; 2117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 547; 765pp; English.
                                                                                                                                                                                                                                                                                                                               Novel human secreted protein #2531.
                                                                                                                                                                    OREISQSLVEKDSLRRQVFEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0552929
2001US-0770160
                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                            WO200179449-A2.
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26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001
                                                                                                                                                                                                                                                                              AAU32040;
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                                                                                                                                                                                                                                                                                                                                          246
                                                                                                  -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                          63 FHEVLRLKDEMLSLS------ LHYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                 586 ATAAE-EREASLRERDAALKQLE-----ALEKEKAAKLEI----LQQQLQVANEARDSA 634
                                                                              10 LQEELN----QEK-----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                             AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                        Mismatches 104; Indels 104;
  Length 2117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Residues_18-2116_of_NuMA
  Score 194; DB 22;
Pred. No. 2.2e-06;
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/label= Coiled_coil_region
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                                    49;
13.3%;
26.6%;
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                      Similarity 26.6
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LexA/NuMA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignant cell growth.
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                                      93;
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The sequences given in AAW21731-32 represent fusion proteins which contain NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interacting proteins (NIE's) (see also AAW21729-30). Compounds which interfere with the interaction of NuMA proliferation. Ab. raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NUMA or NIP, it can be treated by administration of the appropriate functional protein.
proteins - useful for modulating cell division and proliferation and
                                                                          Claim 15; Page 42-50; 78pp; English.
                             in diagnosis
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2192 AA; Sequence

15; 608 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 662 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246 489 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 548 ------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186 63 FHEVLRLKDEMLSLS------ 103 -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145 Gaps 10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62 Query Match 13.3%; Score 194; DB 18; Length 2192; Best Local Similarity 26.6%; Pred. No. 2.3e-06; Matches 93; Conservative 49; Mismatches 104; Indels 104; 247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282 146 187 712 104 q qq g g ò qq δ ò οy ò ò

Search completed: January 22, 2003, 08:52:16 Job time : 63.4933 secs

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US-08-466-390-4
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                                                      January 22, 2003, 08:52:30; Search time 20.2218 Seconds
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                                                                                                   1462
1 ECLAGAIGSLQEELNQEKGQ......TQLRQLQAEPPGVLKQEART 295
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-742-923A-6
US-08-533-306A-4
US-08-742-923A-4
US-08-477-831C-2
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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-08-468-576B-17
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US-09-572-191-2
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US-08-353-700-1
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                                                                                          US-09-767-215-2_COPY_126_420
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Maximum Match 100%
Listing first 45 summaries
                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Sequence 3, Appli
Patent No. 5210183
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appl
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                                                                                                                                                         1, A
85,
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APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 194; DB 1; Length 2101; 26.6%; Pred. No. 9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110

ZIP: 02110

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMT APPLICATION DATA:
             US-09-723-262-2
US-09-723-219-2
S210183-3
US-08-402-217A-3
US-08-95-654-3
US-08-95-658-1
US-08-282-845-2
US-08-282-845-2
US-08-282-845-2
US-08-282-845-2
US-08-282-845-2
US-08-38-105-3
US-08-685-871-2
US-09-310-187A-1
US-09-154-750A-85
US-09-154-750A-85
US-09-085-199B-11
US-09-085-199B-11
US-09-592-054-2
US-09-370-838-191
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                                                                                                                                                                                                                                                       ALIGNMENTS
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STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTP-013
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION UNDRER: 27,829-
REFERENCE/DOCKET NUMBER: MTP-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08466390 Patent No. 5686562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2101 amino acids
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; MOLECULE TYPE: protein
US-08-466-390-4
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ADDRESSEE: TESTA, HI
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08467781
Patent No. 5780596
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(617) 248-7100
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US-08-467-781-4
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                                                                                      QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530
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                                                                                                                                                                                                                    :: || | :|: || 471 | 472 VLQLETLKQEAATLAANNTQLQARVEMETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
                                                     10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
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                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2101;
                                                                                                                                                                                                                                                                    -----TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; Score 194; DB 1; 26.6%; Pred. No. 9.6e-08; iive 49; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/470,950 FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION UNMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-C
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08470950 Patent No. 5698439
                                                                                                                                                                                                                                                                      OREISQSLVEKDSLRRQVFEL---
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Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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472 OSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530
                                                             ---NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                   531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                              187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                               412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2101;
                                                                                                                                                                                                                                                            247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                   SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATONEY/AGENT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: TOUKATIX, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYL
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 194; DB 26.6%; Pred. No. 9.6e tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
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                        531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL
                                                                             AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2101;
                                                                                                                                                          247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%; Score 194; DB 2; 26.6%; Pred. No. 9.6e-08; Live 49; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENT PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NIMBER: US/08/483,924 FILING DATE: 07-JIN-10-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTP-013
                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08483924
Patent No. 5882876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2101 amino acids
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Best Local Similarity 26.6%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-483-924-4
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    146
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-----NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER
                                     531 KOAOLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL
                                                                             AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
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                                                                                                                                                                                                                                                                                                                                GENERAL INCORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: TOUKATLY, GARAMAP
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA HURMITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LHYSNALQEKELAASRCRSLQEELYL---
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                                                                                                                                                       247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                | ::|: || | |:| || | OTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.3%; Score 194; DB 1; 26.6%; Pred. No. 9.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICALL:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECHONE: 617/248-700
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08195487 Patent No. 5783403
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Best Local Similarity 26.6
Matches 93; Conservative
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MOLECULE TYPE: protein
US-08-195-487-4
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US-08-195-487-4
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Sequence 1, Application US/09452294
Patent No. 6287790
GREERLI INFORMATION:
APPLICANT: Lelievre, Sophie
APPLICANT: Bissell, Mina
TITLE OF INVENTION: THERAPH AND DETECTION OF PROLIFERATIVE AND
TITLE OF INVENTION: DIFFERRYIATION DISORDERS
FILE REFERENCE: IB-1454- Sequence Submittal
Patent No. 6287790
CURRENT APPLICATION NUMBER: US/09/452,294
CURRENT FILING DATE: 1999-11-30
DETECTION FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 VLOLETLKOEAATLAANNTOLOARVEMLETERGOGEAKLLAERGHFEEEKOOLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 ------LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                   187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 2101; 9.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 QREISQSLVEKDSLRRQVFEL-------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 QTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                    247 QREISQSLVEKDSLRRQVFEL------TDQVCELRTQLRQLQ 282
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 194; 26.6%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9306160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.3
Best Local Similarity 26.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 2101
                                                                                                                                                                                         RESULT 6
US-09-452-294-1
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T reci, Ozlem; Sahin, Ugur; Pfreundschuh, Michael
VENTION: Methods For Diagnosis And Treating Cancers,
VENTION: And Methods For Identifying Pathogenic Markers In A Sample
VENTION: No. 6232460mal Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S31 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL----- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: || | :|: || 412 VLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 ------LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 -------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 104; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 QREISQSLVEKDSLRRQVFEL-------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ::|: || | |:| || QTSVTQAQVAELALSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQ 684
                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 194; DB 5;
Pred. No. 9.6e-08;
ADDRESSEE: TESTA HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Fulbright & Jaworski LLP
666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELEPHONE: 617/248-7100
TELEPAX: 617/248-7100
                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09104324B Patent No. 6232460 GENERAL INFORMATION: APPLICANT: T reci, Ozlem; Sahin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2101 amino acids
                                                                                                                                                                 Floppy disk
                   53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MELTITLE OF INVENTION: And TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein PCT-US93-06160-4
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                              USA
                                               BOSTON
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US-09-104-324B-4
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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US-08-353-700-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 YYSKEVKDLKTEL-----ENEKLKNTEL-TSHCNKLSLENKELTQE-----TSDMTLE 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAE-------KDILEQSLDE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMA----CQLYREKVNA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 VKCKLDKSEENCNNLRKQV----ENKNKYIEELQQENKALKKKGTAESKQLNVYEIKVNK 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| : |:|| || :| :| || 434 EELKKVLGEKETLLYENKQFEKIAEELKGTEQELIGLLQAREKEVHDLEIQLTAITTSEQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 EELNQEKGQKEVLLRRCQQL-----QEHLGLAETRAEGLHQLEADHSRMKREVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-328-254-6
Sequence 6, Application US/08328254
Sequence 6, Application US/08328254
GENERAL IN-5710022
GENERAL IN-5710022
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFE---LTDQVCELRTQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 176.5; DB 4;
23.9%; Pred. No. 1.1e-06;
tive 53; Mismatches 112;
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....nut.sss:
....nut.sss:
STREET: Campbell and Flores
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION: 435
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: HARSON, NO. 6232460man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
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Matches 71; Conservative
New York
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1787 ENILQEKEQEKVQMKEKSSTAMEMLQTQLKELNERVAALHNDGEACKAKEQNLSSQVECL 1846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ELQEQSLRTASDQ--------ESGDEELNRLKEENEKLRSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 FSLAEKD----ILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 OKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS------QSLVEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08353700
Patent No. 559919
GENERAL INFORMATION:
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: TRANSIBMILY EXPRESSED KINETOCHORE PROTEIN, TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: DANN, DORFMAN, HERRELL AND SKILLMAN 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.9%; Score 173.5; DB 1;
Best Local Similarity 22.4%; Pred. No. 5.9e-06;
Matches 89; Conservative 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2026 KSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREE 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 DSLRRQVFELTDQVCELRTQL---RQLQAEPPGVLKQE 292
       CUBRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 08/141,239
FILING DATE: 22-OCT-1933
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 9-CJ 1191
FELECOMMUNICATION INFORMATION:
TELEPAN: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
24-OCT-1994
N: 435
                                                                                                                                                                                                                                               P-CJ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVSAHFHEVLRLKDEMLSLSLH----
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
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1601 Market Street
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 SNALQEK-----NMVSSCE-L 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS------QSLVEK- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2515 ENILOEKEOEKVOMKEKSSTAMEMLQTQLKELNERVAALHNDGEACKAKEONLSSQVECL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 FSLAEKD----ILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                              COMPUTER: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 11.9%; Score 173.5; DB 1; Best Local Similarity 22.4%; Pred. No. 8.3e-06; Matches 89; Conservative 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2754 KSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREE 2791
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                                                                                                                                        FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION UNMBER: 36,252
TELECOMMUNICATION: TELEPHONE: (215) 563-4100
TELEPRAX: (215) 563-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 emino acids
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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2515 ENILOEKEGEKVOMKEKSSTAMEMLOTQLKELNERVAALHNDQEACKAKEQNLSSQVECL 2574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2575 ELEKAQILIQGLDEAKNNYIVLQSSVKGLIQEVEDGKQKLEKKDEEISRLKNQIQDQEQLV 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNALQEK-----NMVSSCE-L 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ESGDEELNRLKEENEKLRSLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 FSLAEKD-----ILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS------QSLVEK- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLE-----ADHSRMK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2635 SKLSQVEGEHQLWKEQNL-ELRNLTVELEQKIQVLQSKNASLQDTLEVLQSSYKNLENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3248;
                                                                  ZIE: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 173.5; DB 5; 22.4%; Pred. No. 8.3e-06; tive 66; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2754 KSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREE 2791
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                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 REVSAHFHEVLRLKDEMLSLSLH------
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Patent No. 5906819
GENERAL INFORMATION:
APPLICANT: Kalbuchi, Kozo
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPRIONE: (215) 563-4010
TELEPRIX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3248 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                   USA
                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-08-685-576-1
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::::||| :::||| 322 SLEADLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQ--- 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NEKLRSLTFSLAEKDI 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 KLHEMEGAVKSKFKSTIAALEAKIAQLEEQVEQEAREKQAATKSLKQKDKKLKEILLQVE 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 QEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLK 70
                                                                                                                                                                                           APPLICANT: Liu, Pu
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Siciliano, Markers for Detection of Chromosome 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELLOADIOATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828 CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 MVSSCELELQEQSLRTASDQESGDEELNRLKEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2115-00869COB TELECOMMUNICATION INFORMATION: TELEPHONE: (810) 641-1600 TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO: 2:
                                            921 KADSEQLARSIAE -- EQYSDLEKEKIMKELE 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                   Sequence 2, Application US/08533306A Patent No. 5837457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-533-306A-2
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                           Patent No. 5837457 GENERAL INFORMATION:
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                                                                                                                               US-08-533-306A-2
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                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TASDQESGDEELN- 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 REQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.7%; Score 171; DB 2; Length 138
Best Local Similarity 22.1%; Pred. No. 4.7e-06;
Matches 73; Conservative 67; Mismatches 115; Indels
APPLICANT: Nakano, Takeshi
APPLICANT: Ito, Masaaki
APPLICANT: Too, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROFEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLOW ' ' STREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 LKMSEKOLKQENNHLLEMKMSLEKQNAELRKERQDADGQMKELQDQL-
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                       SSEE: Foley & Lardner F: 3000 K Street, N.W., Suite 500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 LVEKDSLRRQVFELTDQVCELRTQ--LRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/843
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)572-5300
TELEPHAX: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PULCASSIFICATION: 435
PULCASSIFICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/685,576
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ANMVSSCELELQEQSLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-685-576-1
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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20007-5109
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEQSLDEARGSRQELVERIHSLRERA-----VAAERQREQYWEEKEQTILQFQKSKMAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: | | :| :| | :| | 321 | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QL-----YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
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                                                                                                                                                         APPLICANT: Liu, Pu
APPLICANT: Liu, Pu
APPLICANT: Liu, Pu
APPLICANT: Siciliano, Michael J.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 3683
REFERENCE/DOCKET NUMBER: 2115-00869DVC
TELEPHONE: (810) 641-050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVSSCELELQEQSLRTASDQESGDEELNRLKEE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRRQVFELTDQ-----VCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/742,923A FILING DATE: No. 5869611ember 1, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                Sequence 2, Application US/08742923A Patent No. 5869611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 21.0°
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC of OPERATING SYSTEM:
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Bloc
STATE: MI
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                                  US-08-742-923A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 DEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQ--------RAN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 MVSSCELELQEQSLRTASDQESGDEELNRLKEE------NEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 LEQSLDEARGSRQELVERIHSLRERA-----VAAERQREQYWEEKEQTLLQFQKSKMAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 LEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKNESARQQ-LERQNKELRS 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 QL------YREKVNALQAQVCELQKERDQAYSARDSAQREISQS-----LVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             502 GDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELEDARASRDEIFATAKENEKKAK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 RDEQNEEK-----RR--QLQRQLHEYET-----ELEDERNERALAAAAKK--KLE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 QEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLK 70
                                                                                                                         APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.6%; Score 170; DB 2; Length 81 Best Local Similarity 21.0%; Pred. No. 2.9e-06; Matches 70; Conservative 73; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                            ADDRESSEE: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828 CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 SLRRQVFELTDQ-----VCELRTQLRQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
           Sequence 6, Application US/08533306A Patent No. 5837457
                                                               GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SMITh, DEANN F.
REGISTRATION NUMBER: 3668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
US-08-533-306A-6
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Search completed: January 22, 2003, 08:57:35 Job time : 28.2218 secs

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January 22, 2003, 08:49:35; Search time 11.8952 Seconds (without alignments) 500.428 Million cell updates/sec
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1462
1 ECLAGAIGSLQEELNQEKGO.....TQLRQLQAEPPGVLKQEART 295
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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//cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	200	% Query Match	% Query Match Length DB	ä	Ę	000001
		11000		3	at a	pesci ipcion
1	1462	100.0	1004	10	US-09-767-215-2	Sequence 2, Appli
7	1443	98.7	1138	10	US-09-767-215-5	Sequence 5, Appli
e	369	25.2	1247	0	US-10-032-159A-8	Sequence 8, Appli
4	364	24.9	319	σ	US-10-032-159A-12	Sequence 12, Appl
S	198	13.5	366	σ	US-10-032-159A-2	Sequence 2, Appli
9	198	13.5	366	σ	US-10-032-159A-20	Sequence 20, Appl
7	185	12.7	691	σ	US-10-028-072-16	Sequence 16, Appl
80	185	12.7	1597	σ	US-10-017-216-6	6, A
6	185	12.7	1641	0	US-10-017-216-5	Ī
10	185	12.7	2055	σ	US-10-017-216-4	4
11	184	12.6	868	6	US-09-884-001-19	19,
12	183	12.5	1286	σ	US-10-017-216-7	~
13	183	12.5	1958	12	US-10-028-946-4	_
14	183	12.5	2053	σ	US-10-017-216-2	Sequence 2, Appli
15	183	12.5	2054	12	US-10-028-946-2	Sequence 2, Appli
16	177	12.1	2310	6	US-09-991-496-120	
17	177	12.1	2310	10	US-09-874-923-120	Sequence 120, App
18	174.5	11.9	2139	10	US-09-727-384-6	Sequence 6, Appli
19	172	11.8	645	σ	US-09-764-868-625	Sequence 625, App

241 SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART 295

δλ

Sequence 787, App Sequence 305, App Sequence 17, Appl Sequence 16, Appl Sequence 29, Appl Sequence 191, Appl Sequence 191, Appl Sequence 191, Appl Sequence 191, Appl Sequence 8, Appl Sequence 8, Appl Sequence 8, Appl Sequence 44, Appl Sequence 44, Appl Sequence 5, Appl Sequence 219, Appl Sequence 210, Appl Appl Sequence 210, Appl Appl Sequence 210, Appl Sequence 210, Appl Sequence 210, Appl Appl Sequence 210, Appl Appl Sequence 210, Appl Appl Appl Appl Appl Appl Appl App		ά	JEADHSRMKREVS 60                  JEADHSRMKREVS 185	LORANMVSSCELE 120 	AARGSRQELVERI 180 	QVCELQKERDQAY 240 
US-09-925-297-787 US-10-108-605-305 US-09-864-761-47959 US-09-785-770A-16 US-09-915-770A-16 US-09-915-299-988 US-09-915-299-988 US-09-915-299-988 US-09-925-297-740 US-09-925-297-740 US-09-925-297-740 US-09-964-761-38419 US-09-964-761-38419 US-09-976-740-8 US-09-965-988 US-09-965-988 US-09-965-988 US-09-965-988 US-09-976-740-8 US-09-976-740-8 US-09-976-740-8 US-09-976-740-8 US-09-976-740-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8 US-10-023-529-8	LIGNMENTS S OF THE CARD-R AND USES THER 767,215 59 Ion 4.0	; Score 1462; DB 10; Le; ; Pred. No. 2.6e-92; 0; Mismatches 0; Inc	ECLAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVS 	AHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANWYSSCELE 	LQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERI 	HSLRERAVAAERQREOYWEEKEOTLLQFOKSKWACQLYREKVNALQAQVCELQKERDQAY 
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Factor No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: CARD-DOMAIN COLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSLRERAVAAERQRE---------QYWEEKEQTLLQFQKSKMACQLYREKV
18;
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                                                                                                       GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT PAPLICATION NUMBER: 05/09/767,215
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: PRIOR FILING
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                  Score 1443; DB 10;
Pred. No. 5.9e-91;
0; Mismatches 0;
                                                                               Sequence 5, Application US/09767215 Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                     98.78;
94.28;
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 295; Conserv
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US-10-032-159A-8
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                                                                   US-09-767-215-5
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                                                                                                                                                                                        -----163
                                                                                                                                                                                                                                                                                                                                                         164 QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                           : |: || || || 360 TVMLQLEEVERERDQGQAVAFQGHCIKALNTEPATSKGRTIGSVIALMKKAFHSKDEAQT 419
                                                                                                                                                                                                                                              HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                              3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
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Sequence 12, Application US/10032159A

Patent No. US2002016470341

GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2001-12-19
PRIOR PPLICATION NUMBER: US 60/257,457

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 12

SEQ ID NO 12
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                                                                       ; Score 369; DB 9; L; Pred. No. 8.2e-18; 66; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                   122 QEQSLRTASDQES -- GDEELNRLKEENEKLRSLTFSL --
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 102; Conserv
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US-10-032-159A-12
                                       US-10-032-159A-8
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229 VCELQKERDQA 239
                                                                                                                                                                                                          Similarity
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                                                                                                                                                   US-10-032-159A-20
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                                                                            63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
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ELQKERDQ-----AYSARDSAQREISQSLV 255
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR PAPLICATION NUMBER: US 60/257,457
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 366
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Sequence 20, Application US/10032159A

Sequence 20, Application US/10032159A

Sequence 20, Application US/10032159A

GENERAL INFORMATION:
APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Grant-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: P-LJ 5100
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                                                                                                                                                                                                                                                               Sequence 2, Application US/10032159A Patent No. US20020164703A1
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EKDKYRKQIRELEEKNDEMRIE 319
                                                                                                                               EKDSLRRQVFELTDQVCELRTQ 277
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ORGANISM: Homo sapiens
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Matches 67; Conserv
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123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE 168
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                                                                                                                                                                                                                                             Length 366;
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                                                                                                                                                                                                                                                                                                                                           17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS-
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 366
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26.7%;
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
Gao, Wel-Qiang
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                                                                                                                                                                                                                                                                                                67; Conservative
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                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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350 MEEVAIERDQS 360
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PRIOR APPLICATION NUMBER: 60/059184

REIOR FILING DATE: 1997-091.

REIOR FILING DATE: 1997-091.

REIOR PLICATION NUMBER: 66/059263

REIOR PLICATION NUMBER: 66/05936

REIOR PLICATION NUMBER: 66/05337

REIOR PLICATION NUMBER: 66/05334

REIOR RELING DATE: 1997-10-3

REIOR RELING DATE: 1997-11-3

REIOR RELING DATE: 1997-11-3

REIOR RELING DATE: 1997-11-3

REIOR RELICATION NUMBER: 60/05634

PRIOR RELICATION NUMBER: 60/05634

PRIOR RELICATION NUMBER: 60/05634

PRIOR RELICATION NUMBER: 60/05634

PRIOR RELICATION NUMBER: 60/05334

PRIOR RELICATION NUMBER: 60/05334

PRIOR RELICATION NUMBER: 60/05334

PRIOR RELICATION NUMBER: 60/05334

PRIOR RELICATION NUMBER: 1997-11-1

PRIOR RELICATION NUMBER: 1997-11-1

PRIOR RELICATION NUMBER: 1997-11-1

PRIOR RELICATION NUMBER: 1997-11-1

PRIOR RELICATION NUM
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PRIOR APPLICATION NUMBER: 60/074092
PRIOR PLILICA DATE: 1998-0.20
PRIOR PLILICA DATE: 1998-0.3-12
PRIOR FILING DATE: 1998-0.3-20
PRIOR FILING DATE: 1998-0.3-20
PRIOR FILING DATE: 1998-0.3-20
PRIOR PLILING DATE: 1998-0.3-20
PRIOR PLILING DATE: 1998-0.3-20
PRIOR APPLICATION NUMBER: 60/07924
PRIOR APPLICATION NUMBER: 60/08129
PRIOR PLILING DATE: 1998-0.3-31
PRIOR PLILING DATE: 1998-0.3-31
PRIOR PLILING DATE: 1998-0.4-09
PRIOR PLILING DATE: 1998-0.4-14
PRIOR PLILING DATE: 1998-0.4-14
PRIOR PLILING DATE: 1998-0.4-15
PRIOR PLILING DATE: 1998-0.4-16
PRIOR PLILING DATE: 1998-0.4-29
PRIOR PLILING DATE: 1998-0.5-17
PRIOR PLILING DATE: 1998-0.5-17
PRIOR PLILING DATE: 1998-0.5-17
PRIOR PLILING DATE: 1998-0.5-17
PRIOR PLILING DATE: 1998-0.5-13
PRIOR PLILING DATE: 1998-0.5-15
PRIOR APPLICATION NUMBER: 60/08639
PRIOR PLILING DATE: 1998-0.5-15
PRIOR APPLICATION NUMBER: 60/08639
PRIOR PLILING DATE: 1998-0.5-15
PRIOR APPLICATION NUMBER: 60/08639
PRIOR PLILING DATE: 1998-0.5-13
PRIOR APPLICATION NUMBER: 60/08639
PRIOR PLILING DATE: 1998-0.5-13
PRIOR APPLICATION NUMBER: 60/08639
PRIOR PLILING DATE: 1998-0.5-13
PRIOR PRILING DATE: 1998-0.5-13
PRIOR PRIL

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Sequence 5, Application US/10017216
Patent No. US2002016048341
GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13345, A No. US20020160483A1el Human Myotonic Dystrophy Type
FILE PERENEUS: Kinase and Uses Therefor
FILE REFERENCE: 10147-5701
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                                                                                                                                        HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
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                                                                 Gaps
                                                                                                         11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
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                                                                                                                                                                                                   HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS
                                                                                                                                                                                                                                                                                                                                                                                 162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREGYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----QVCELQKERDQAYSARDSAQREI
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                  Length 1597;
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                     12.7%; Score 185; DB 9; 26.5%; Pred. No. 3.6e-05;
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                                                                 Mismatches
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PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
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                                                               Conservative
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                                   Best Local Similarity
Matches 88; Conserv
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Matches 88; Conserv
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US-10-017-216-5
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                       Query Match
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CURRENT APPLICATION NUMBER: US 60/242,429
PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOCTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --RSRLEVAEVNGRLAELGLHLKEEKCQWSKERAGLLQ-----SVEAEKDKILKLSAEI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 CELQK----ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 185; DB 9; 24.9%; Pred. No. 1.4e-05; tive 55; Mismatches 129
         PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091863
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
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Patent No. US20020160483A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/(
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.7%
Best Local Similarity 24.9°
Matches 93; Conservative
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APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type ITTLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type ITTLE OF INVENTION: Kinase and Uses Therefor TITLE OF INVENTION: Kinase and Uses Therefor CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT APPLICATION NUMBER: US 60/242,429
PRICR APPLICATION NUMBER: US 60/242,429
PRICR PELLING DATE: 2001-10-23
NUMBER: OS SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                        QRANMVSSCELELQEQSLRTASDQESG--DEELNRLKEENEKLRSLTFSLAEKDILEQSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEARGSRQELVERIHSLRERAVAAERQRE-----QYWEEKE----QTLLQF 208
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                                                                                                                                                                                                                                                                         ----HYSNALQEKELAASRCRSLQEELYLLKQEL 108
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Best Local Similarity 26.2%; Pred. No. 3.9e-05;
Matches 87; Conservative 55; Mismatches 98; Indels
                                                                                                                                                               Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 ISQSLVEKDSLRRQVFELTDQVC------ELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 184; DB 9; L. 25.9%; Pred. No. 2.1e-05; iive 52; Mismatches 117;
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                 SOFTWARE: Patentin Ver.
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 68 RLKDEMLSLSL----
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 89; Conserv
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NUMBER OF SEQ
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US-10-017-216-7
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                                                            LENGTH:
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Patent No. US20020160483A1
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: 13345, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
TITLE OF INVENTION: Kinase and Uses Therefor
TITLE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
CUBRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.7%; Score 185; DB 9; Length 205
Best Local Similarity 26.5%; Pred. No. 4.8e-05;
Matches 88; Conservative 54; Mismatches 98; Indels
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                                               110 TES------RQVVELA--VKEHKAEILALQ 731
                         251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Mus musculus
US-10-017-216-4
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GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVERTION: No. US20020123622Alel Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                            Length 2053;
                                                                                                                                                                                                                                                                                                                                                             98; Indels
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                                                                                                                                                                                                                                                                                                            12.5%; Score 183; DB 9; 26.2%; Pred. No. 6.6e-05; iive 55; Mismatches 98
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FILE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-33
PRIOR APPLICATION NUMBER: US 60/242,429
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VOS: 7
SOFTWARE: PATENTIN VOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10028946
Patent No. US20020123622A1
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.2%
Matches 87; Conservative
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US-10-028-946-2
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APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Hiranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION WUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
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                           162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY 218
                                                        248 ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 296
                                                                                                                      ----- QVCELQKERDQAYSARDSAQREI 250
                                                                                                                                                                297 EEQVMDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907 HEEQKLELKROLTELQL----SLOERESQLTALQAARA-ALESQLRQAKTELEE----TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- QVCELQKERDQAYSARDSAQREI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1958
                                                                                                                   219 REKVNALQA------
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Patent No. US20020160483A1
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10028946
Patent No. US20020123622A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.2 Matches 87; Conservative
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; ORGANISM: homo sapiens
US-10-028-946-4
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US-10-017-216-2
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US-10-028-946-4
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1016 ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 1064
                                                                                    162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY 218
                                                                          219 REKVNALQA------2007 RELONGENDOAYSARDSAQREI 250
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Search completed: January 22, 2003, 08:52:51 Job time: 17.8952 secs

10:56:38 2003

Wed Jah 22

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version 5
- 2003 C
GenCore
Copyright (c) 1993
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protein search, using sw model OM protein

2003, 08:49:35 ; Search time 22.6008 Seconds (without alignments) 1254.807 Million cell updates/sec January 22, Run on:

US-09-767-215-2\_COPY\_126\_420 1462 1 ECLAGAIGSLQEELNQEKGO.....TQLRQLQAEPPGVLKQEART 295 score: Title: Perfect :

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 0B 0B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		trichohvalin - rah	1.10	- mouse	nqn	centromere protein	- (1		ome as	-	<u>-</u>	•	olq	myosin heavy chain	myosin II heavy ch	etical pro	- human	٠	hea	kinesin-related pr	- w		qiantin - human		2	e myos	mvosin heavy chain		<b>^</b>	nonmuscle myosin I
SUMMARIES	ID	S28589	18	T30171	T13030	S28261	T22976	T26101	T08621	G02520	A59404	S68420	JC5837	S21801	T47237	T16507	152300	A39638	A59252	T14156	A59236	A33977	A56539 .	T14265	804090	C84788	A47297	T14867	138055	5928
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ď	Query Match	13.9	13.3	13.1	13.1	12.9	12.9	12.8	12.8	12.7	12.7	12.7	12.7	12.6	12.6	12.5	12.4	12.4											12.0	
	Score		194	192	191.5	188.5	188	187.5	186.5	185.5	185.5	185	185	184.5	184	182.5	181.5	181.5	181	181	180.5	180.5	179.5	178.5	178.5	177		175.5	175.5	175
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	outer dense fiber	hypothetical prote	trichohyalin - she	myosin heavy chain	myosin heavy chain	myosin heavy chain	gene retil protein	protein kinase (EC	transport protein	hypothetical prote	myosin heavy chain	_	SCP1 protein - rat	C	cell-cycle-depende
B43402	T03791	T33318	A40691	A24922	T18296	S06117	138153	T14039	S67593	T21174	A61231	148176	S28061	S49461	PC4035
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2007	638	14/5	1549	1940	2139	924	899	1732	1790	2020	1961	845	946	993	1017
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175	174.5	1/3.5	173.5	173.5	173.5	173	172.5	172.5	172.5	172.5	172	171.5	171.5	171.5	171.5
30	3.2	25	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus
C.Species: Oryctolagus
R.Fietz, M.J.; Rogers, G.E.
Submitted to the EMBL Data Library, December 1992
R.Fietz, M.J.; Rogers, G.E.
A.Description: Examination of the gene encoding rabbit trichohyalin.
A.Reference number: 528589
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-1407 <FIES
A.Molecule type: DNA
A.Residues: Trichohyalin is a protein of the medulla of the hair and of the inner root C.Comment: Trichohyalin is a protein include conversion of arginine to citrulline a C.Genetics: 46/3
C.Genetics: 46/3
C.Superfamily: trichohyalin; calmodulin repeat homology
C.Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F.49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 EQELRQERERKLREEEQLLRREEQ------ELRQERERKLREEEQLLQEREEBRLRRQ 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD-------QAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1407;
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Pred. No. 0.0011;
8; Mismatches 108;
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27.7%; Pre-
tive 48;
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Matches 97; Conservative
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RESULT

Ricantz, V.A.; Miller, K.G. J. Cell Biol. 140, 897-910, 1998 A:Title: A class VI unconventional myosin is associated with a homologue of a microtu A;Reference number: 217588; MUID:98139549; PMID:9472041 A.Cross-references: EMBL.AF041382; NID:92773362; PID:92773363; PIDN:AAB96783.1 A.Experimental source: strain Oregon R microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000 C; Accession: T13030 A;Accession: T13030 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1690 <LAN> A;Cross-references: FlyBase:FBgn0020503 C;Keywords: cytoskeleton Best Local Similarity C; Accession: T30171 Query Match Best Local Simi Matches 84; - mouse Query Match C; Genetics: 146 9 259 RESULT 4 ninein q Q Op q ΩD qq Qγ δ ò Qγ ΟŊ δ q Availed mitotic apparatus protein NuMA - Numan Chicler mitotic apparatus protein NuMA - Numan Chicler mitotic apparatus protein NuMA - Numan Chicler mitotic apparatus protein NuMA - Number 13 - Numb 15; 186 |:||::|: | | ||:||:472 QSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTTLNATIQQQ-DQELAGLKQQAKE 530 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246 531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585 ATAAE-EREASLRERDAALKQLE----ALEKEKAAKLEI----LQQQLQVANEARDSA 634 362 LEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS------QLQDNPPQEKGEVLGD 411 412 VLOLETLKQEAATLAANNTQLQARVEMLETERGQQEAKLLAERGHFEEEKQQLSSLITDL 471 LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62 ---NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER Length 2101; ---LHYSNALQEKELAASRCRSLQEELYL------TDQVCELRTQLRQLQ 282 Indels 13.3%; Score 194; DB 2; 26.6%; Pred. No. 0.0049; tive 49; Mismatches 104 247 QREISQSLVEKDSLRRQVFEL--FHEVLRLKDEMLSLS----Best Local Similarity 26.6 Matches 93; Conservative Query Match 10 63 187 586 146 g g d ò g ò qq ò ò

Length 1690;

.; ?

Score 191.5; DB Pred. No. 0.0053;

13.1%; 21.4%;

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R; Bouckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; Mil J. Cell Sci. 109, 179-190, 1996
A; Title: Molecular characterisation of ninein, a new coiled-coil protein of the central A; Reference number: 220751; MUID:96431720; PMID:8834802
A; Accession: T30171
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-2168 <BOU>
A;Cross-references: BMBL.40342; NID:g1113864; PID:g1113865; PIDN:AAA83234.1
A;Experimental source: strain C57B1/6
A;Experimental source: strain C57B1/6
A;Note: localised specifically in the pericentriolar matrix of the centrosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 -LQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS-----QSLVEKD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 RMKREVSAHFHEVLRLKDEMLSLSLHYSNAL-QEKELAASRCRSLQEELYLLKQEL---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIGSLQ-EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL------HQLEADHS 53
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| ::|: || || || || || 635 QISVIQAQNEKAELSRKVEELQACVETARQEQHEAQAQVAELELGLRSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision
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34; Conservative
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Oy 120 ELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQS 165	RESULT 6 122976 hypothetical protein F59A2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T22976; T23157 R;Lightning, J. Submitted to the EMEL Data Library, June 1994 A;Reference number: 219645 A;Accession: T22976 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1133 <wil> A;Residues: 1-1133 <wi< th=""><th>A:Status: preliminary; translated from GB/EMBL/DDBJ A:Nolecule type: DNA A:Residues: 1-133 AM2&gt; A:Ross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6 A:Cross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6 A:Experimental source: clone K01A11 C;Genetics: A:Genetics: A:Genet</th><th>  Qy   41RAEGLHQLEADHSRMKREVSAHFHEVLRIKDEMISIS 77   1   1   1   1   1   1   1   1   1</th></wi<></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil>	A:Status: preliminary; translated from GB/EMBL/DDBJ A:Nolecule type: DNA A:Residues: 1-133 AM2> A:Ross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6 A:Cross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6 A:Experimental source: clone K01A11 C;Genetics: A:Genetics: A:Genet	Qy   41RAEGLHQLEADHSRMKREVSAHFHEVLRIKDEMISIS 77   1   1   1   1   1   1   1   1   1
GSLOBELNOEKGOKEVLLRRCQOLQEH	2054 720 720 725 780 257 289 898 898	S28201 S28201 S28201 N.Alternate protein E - human N.Alternate names: centromere 312K protein; kinesin-related protein CENP-E C; Species: Homo saptens (man) C; Date: 103-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001 C; Accession: S28201 R; Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W. Nature 359, 536-539, 1995 A; Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis. A; Reference number: S28201; MUID:93024922; PMID:1406971 A; Accession: S28201 A; Modecule type: mRNA A; Residues: 1-2663  A; Residues: 1-2663  A; Cross-references: EMBL:215005; NID:929864; PIDN:CAA78727.1; PID:929865 A; Cross-references: GDB:361164; OMIM:117143	A wap position: 424-4424  A wap position: 424-4424  C; Superfamily: centromere protein E; kinesin motor domain homology  C; Keywords: ATP; colled coil; microtubule binding; mitosis; nucleotide binding; F; 7-35/Domain: kinesin motor domain homology kmory  E; 7-35/Domain: kinesin motor domain homology kmory  F; 86-93/Region: nucleotide-binding motor formain homology  E; 86-2183/Domain: colled coil #status predicted kmory  E; 86-2183/Domain: colled coil #status predicted kmory  E; 92/Binding site: ATP (Lys) #status predicted kmory  E; 92/Binding site: ATP (Lys) #status predicted  Query Match  Query Match  Best Local Similarity 24.2%; Pred. No. 0.012;  Matches 77; Conservative 50; Mismatches 110; Indels 81; Gaps 12;  Matches 77; Conservative 50; Mismatches 110; Indels 81; Gaps 12;  QY 3 LAGAIGCALORELNORKGOKEVLLRRCOQLOEHLGLAETRAEGLHOLEADHSRAKREV

; 710/3; 738/3; 795/2; 1008/3

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QT 796
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C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08621
A:Title: Autcantibodies to a group of centrosomal proteins in human autoimmune sera A:Reference number: 216462: MUID:98165428; PMID:9506584
A:Reference number: 216462: MUID:98165428; PMID:9506584
A:Reference number: 216462: MUID:98165428; PMID:9506584
A:Recession: T08621
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Rolecule type: man.NA
A:Residues: 1-2442 < MAC>
A:Residues: 1-2442 < MAC>
A:Residues: 1-2442 cMAC>
A:Coss: references: EMBL:AF022655; NID:q2832236; PIDN:AAC06349:1; PID:g2832237
A:Experimental source: cell line HeLa
                                                                           Typothetical protein W02B8.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Toact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T26101
R.Sims, M.
submitted to the EMBL Data Library, October 1996
A.Reference number: 220151
A.Reference number: 220151
A.Reference number: 220151
A.Reference specifical narry; translated from GB/EMBL/DDBJ
A.Rocession: T26101
A.Residues: 1-1256 ANIL>
A.References: EMBL: 281136; PIDN: CAB03458.1; GSPDB: GN00209; CESP: W02B8.2
A.References: CESP: W02B8.2
A.References: EMBL: 237/3; 670/3; 949/3; 1073/3
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Best Local Similarity 24.6%
Matches 89; Conservative
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A.Gene: PLEC1
C.Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protei
F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>
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A;Residues: 1-4574 <MCL>
A;Cross-references: EMBL:U53204; NID:g1477645; PIDN:AAB05427.1; PID:g1477646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C.Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C.Accession: G02520
R.McLean, W.H.I.; Smith, F.J.D.
Submitted to the EMBL Data Library, March 1996
A.Reference number: H01385
A.Recession: G02520
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 | 1:1: | :: | 11 | :- | 1206 SAEAERLKLRVAEMSRAQARAEEDAQRFRKQAEEIGEKLHRTELATQEKVTLVQTLEIQR 2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2466 QQSDHDAER---LREAIAELEREKEKL--QQEAKLLQLKSEEMQTVQQEQLLQETQALQQ 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: | ||:|| |: || sflsendellorrengerakleqlevakaqqlreeqqrqqqqqreerreeqqrqqqqqreeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2293 LOEEAEKMKOVAEEAARLSVAAQEAARLROLAEEDLAQORALAEKMLKEKMOAVQEATRL 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SLRTAS---DQESGDEELNRLKEE----NEKLRSLTFSLAEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQVCE----LQKER------ Z60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                       --SLVEKDSL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                      RRQ--VFELTDQVCE----LRTQLRQLQA---------------EPPGVLKQEA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LQRANMVSSCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLA-EKDI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69
                                                                                                                                                                                                -----EVADLRAAAVKLSALNEALALDKVG
                                                                                                                                                                                                                                                                    162 LEQSL-----DEARGSRQELVERI-HSLRERAVAAERQREQYWEEKEQTLLQFQKSKMA
                                                             505 GOKEEQQEELHLAVRERERLQEMLMGLEAKQSESLSELITLREALESIHLEGELLRQEQT
-MKREVSAHFH----EVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%; Score 185.5; DB 2;
ilarity 27.0%; Pred. No. 0.032;
Conservative 41; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                   215 CQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 -- RRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                                                                                                                565 EVTAALARAEQ-SIAELSSSENTLKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δy
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:   :      : : :   :   :    :	0y 62 HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSS 116	12  191 complex-associated profess: Rattus norvegicus (Norvo 05-Mar-1998 #sequence_rev. sion: JC5837  102. Fullwara, T.; Sohda, Fuct. Funct. 22, 565-577, i. Identification and charaence number: JC5837; MUID: Sin nucleic acid sequence nule type: mRNA  10. 13187 < TOK  10. This protein plays a rafarences: DBB:D25543; int: This protein plays a rafarences: DBB:D25543; int: This protein plays a rafarences: DBB:D25543; int: This protein plays a rafamily: glantin  3.187/Domain: membrane anch. Match. 25, 21, 21, 21, 21, 21, 21, 21, 21, 21, 21	Best Local Similarity 25.3%; Pred. No. 0.023;     Matches 82; Conservative 54; Mismatches 98; Indels 90; Gaps 13;     Oy 7 IGSLOBELNOEKOG
Db 2581 EARRQHEAEEGVRRKQEELQQLEQQ 2606	RESULT 10 A59404 Discrim [imported] - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002 C;Accession: C59404, A53404 Fritu: unman plectin: organization of the gene, sequence analysis, and chromosome loca A;Title: unman plectin: organization of the gene, sequence analysis, and chromosome loca A;Reference number: C59404 A;Reference number: C59404 A;Reference speciminary A;Reference speciminary A;Molecule type: DNA A;Residues: 1-4684 <sto> A;Cross-references: GB:CAA91196; NID:g1296662; PIDN:CAA91196.1 C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S Query Match Best Local Similarity 27.0%; Pred. No. 0.032; Matches 88; Conservative 41; Mismatches 134; Indels 63; Gaps 11;</sto>	OY 10 LOEELNOEKGGKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL 69  1111 :	PESULT 11 S.6812  RESULT 11 S.68420 C.Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999 C.Accession: S68420 C.Accession: S

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A; Cross-references: EMBL: U41994; NID: 91123047; PID: 91123050; PIDN: AAA83454.1; CESP: F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appothetical protein F59A6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
            C;Species: Naegleria fowleri
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 EQSLIDEARGSRQELVERIHSL----RERAVAAERQREQYWEEKEQTILIQFQKSKMACQLY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 TQKKNDADNRVKQLESELQGVKSERDRLNKDLNNTSGDMNGLKRQLDESNNLVAKLKAEI 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 VNLLEDDLKHHQSQIRILQNKCSTLEMEKQTLQETIQRAQDDKKETETELESSRSRLHVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 MLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL----QRANWVSSCELELQEQSL-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RLKEENEKLR----SLTFSLAEKDIL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSLDSKVKSLEDKIRELTALLETERSSKTDLDKKRSKMDKEVKRLAQQLQETEQALKGE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IGSLQEELNQEKGQKEVLLRRC-----QQLQEHLGLA-ETRAEGLHQLEADHSR---M 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRLKDE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 REKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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myosin II heavy chain [imported] - Naegleria fowleri (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.6%; Score 184; DB 2; Length 74 Best Local Similarity 21.2%; Pred. No. 0.0058; Matches 65; Conservative 73; Mismatches 130; Indels
                                                                                                                R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, submitted to the EMBL Data Library, December 1995 A;Description: Codon usage in Naegleria fowleri. A;Reference number: 224413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nhan, M. submitted to the EMBL Data Library, December 1995 A;Description: The sequence of C. elegans cosmid F59A6. A;Reference number: 218526 A;Reference number: 218506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 182.5; DB 2;
Pred. No. 0.012;
9; Mismatches 119;
                                                                                                                                                                                                                                      A, Accession: T47237
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1.746 < SHA>
A, Cross-references: EMBL:U43192; PIDN:AAB01786.1
A, Experimental source: strain LEE mp; cell type amoeba
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A;Introns: 35/3; 335/3; 685/3; 973/3; 1097/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Sco
24.0%; Pre
tive 69;
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A; Residues: 1-1286 <NHA>
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les 76; Conserv
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328 QKLQKD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQLQAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T16507
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A; Gene: CESP:F59A6.
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Matches
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B;Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral A;Reference number: PN0013; MUID:91151356; PMID:1998509
A;Recession: PN0013; MUID:91151356; PMID:1998509
A;Recession: PN0013
A;Molecule type: mRNA
A;Residues: 1914-1998,'I' <SU2>
A;Residues: 1914-1998,'I' <SU3>
A;Residues: 1914-1998,'I' <SU3-1999,'Region: 11944 meromyosin
                                                               N'Alternate names: myosin II
N'Contains: myosin ATPase (EC 3.6.4.1)
N'Contains: myosin ATPase (EC 3.6.4.1)
C'Species: Rattus norvegicus (Norway rat.)
C'Species: Rattus norvegicus (Norway rat.)
C'Accession: S21801; PN0013; S18134
C'Accession: S21801; PN0013; S18134
J. Mol. Biol. 224, 1185-1193, 1992
A'Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain A'Reference number: S21801; MUID:92235856; PMID:1569576
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ف
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1758 QIDQINADLNLERGHAQKNENARQQLERQNKELKVKLQEMEGTVKSK-----YKASITAL 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1813 EAKIAQLEEQLDNETKERQAACKQVRRTEKKLKDVLLQVDDERRNAEQYKDQADKASTRL 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAQVCELQKERDQAYSARDSA-----QREISQSLVEKDSLRRQVFELTDQVCELRTQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EELNRLKEE------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSL-- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AEGLHQLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1277-1999/Region: light meromyosin
F;125/Modified site: N6.N6.trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 184.5; DB 19.4%; Pred. No. 0.015;
                                       osin heavy chain, neuronal [similarity] - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETR--
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A, Molecule type: mRNA
A, Residues: 1-1999 <SUN>
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B_CHICK P10587 gallus gall B_HUMAN P5597 mus musculu 0_MOUSE 0_00547 mus musculu 0_RACAA P05559 carthamoeb P35458 gallus gall C_MOUSE P35458 gallus gall P48678 mus musculu P48678 mus musculu P48679 musculu P48679 musculu P48679 musculu P48679 musculu P48679 mu	IRE_HUMAN STANDARD; PRT; 1004 AA.  CARE_HUMAN STANDARD; PRT; 1004 AA.  O9BXL6; O9BVB5;  15-JUN-2002 (Rel. 41, Last sequence update)  15-JUN-2002 (Rel. 41, Last annotation update)  Caspase recruitment domain protein 14 (CARD-containing MAGUK protein 2).  CARD14 OR CARMA2.  CARD14 OR CARMA1.  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MAGUK protein 2.  MAGUK PRIMATOR (Human).	M.D., Poyet JL., ano P.S., Alnemri E.S.; recruitment domain kinase (MAGUK) family members e NF-kappaB.";	Bonnet D., Thome M., Tschopp J.; j partner of Bcll0, induces Bcll0 [vation."; Bonnet D., Thome M., Tschopp J.;	SEQUENCE OF 1-740 FROM N.A.  SISSUB-CECEVIX, and Colon; Strausbeeg R.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.	long as its content is in no
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напапапапап	eate st s st a in p data	112 Y., Y., Ovel ovel and -118	ed=113561 Micheau Jing bind -KappaB a (2001). Micheau (2001).	The state of the s	tit
1978 1972 1972 1325 1087 1509 1224 574 665 1130	ANDARD; 41, Cr 41, La 41, La 61, La an: doma	PubMed ., Guo Merria 4 are n ssociat h Bc110 6:11877	PubMed n F., M ontaini nd NF-k 1-127(2 n F., M 8-198(2	11-740 FROM N.A.  "x, and Colon;  EC-2000) to the left of the left	it ins
11.7 11.7 11.6 11.6 11.5 11.5 11.5 11.5 11.5 11.5	ST. 3VB5; (Rel.,	XOM N.A 192234; Wang L a S.M., d CARD1 orane-a act wit hem. 27	IN=21225663; promed, a Carbinon mal, a Carbinon phorylation and Lett. 496:121-TUM. e O., Martinon Lett. 505:198-	ENCE OF 1-740 FROM USBECEVIX, and Colusbecevix, and Columbication, an	non-prof
171.5 170.5 170.5 170.5 170 170 168.5 168.5 168.5 168.5	T. 1 CARE_HUMAN CARE_HUMAN Q9BXL6; Q99 115-JUN-200; 115-JUN-200; Caspase rec Caspase rec 2) (Carma 2) (Carma CHOMO Sapier HOMO Sapier HOMO Sapier HOMO HOMO HOM	COUENCE FI COUENCE FI COUENCE 21. Inivasula. ARD11 and ARD11 and ARD11 and Biol. Cl	MEDLINE-21250563; PubMed-11356195; Gaide O., Martinon F., Micheau O., B "Carmal, a CARD-containing binding phosphorylation and NF-kappaB activa FBBS Lett. 496:121-127(2001).  [3] BRRATUM. [3] Gaide O., Martinon F., Micheau O., B FEBS Lett. 505:198-198(2001).	SEQUENCE OF 1-74 TISSUBE-Cervix, a Strausberg R: Submitted (DEC-2	рÀ
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rattus norv

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homo sapien

mus musculu

P25386 Q60563 Q62209 Q03410

CENF\_HUMAN USO1\_YEAST SCP1\_MESAU

MYH4\_HUMAN MYH9\_HUMAN TRHY\_SHEEP

MYH8\_HUMAN

gallus gall homo sapien homo sapien

MYH3\_HUMAN MYH9\_RAT SCP1\_HUMAN GOG4\_HUMAN

\_CHICK\_HUMAN

MYHD\_

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CARB_HUMAN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MACUK protein
                                                                                                                                                                                                                                            DYEASEPLEKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
GYRKLLODLEAK -> SRARPLLSPGLLMGTVAAGGYTQAD
FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
AAH01326).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365
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                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                              Length 1004;
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MEDLINE-21391892; PubMed-11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
Lii Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                         7469B8B56BE06073 CRC64;
                                                                                                                                                                                                          COILED COIL (POTENTIAL)
                                                                                                                                  PROSITE; PS50209; CARD: 1.
PROSITE; PS50209; CARD: 1.
PROSITE; PS500106; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
Coiled coil. 15 107 CARD.
DOMAIN 128 409 COILED COIL (POTENTIAI DOMAIN 568 658 PDZ.
DOMAIN 858 990 GUANYLATE KINASE.
CONFLICT 619 671 DYEASEPLFRAVLEDTILEEAN
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Pred. No. 3.8e-71;
0; Mismatches 0;
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                                          EMBL, AF322642; AAG53403.1; -.
EMBL, AV032927; AAK54453.1; -.
EMBL, BC018142.3; -.
EMBL, BC001326; AAH18142.1; -.
EMBL, BC001326; AAH01326.1; AIT_INIT.
INTERPRO; IPRO00619; Guanylate_kin.
INTERPRO; IPRO1478; PDZ.
SMART; SM00072; GuKC; 1.
SMART; SM000228; PDZ.
                                                                                                                                                                                                                                                                                                              100.0%;
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Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                          1004 AA;
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CARD14 OR BIMP2.
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                                                                                                                                                                                                                                                                                           SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and prosperit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 SRERSLKMASNLEPQGEELNRLKEENEKLRSMTFSLVEKDILEQSLDEARESKQELVDRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 TARDRAQMEISQRLVEKDALRRRVFELTEQVCELRTQLRRLQAEAPGGPKQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 743 QAQQQLLA -> HLLEDHRS (IN R)
999 AA; 113496 MW; D18350DA12430255 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.8%; Score 1166; DB 1;
79.9%; Pred. No. 2.1e-55;
iive 29; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE KINASE_1; FALSE_NEG.
PROSITE; PS50106; PD2; 1.
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
Bc110-mediated NF-kappa B induction.";
J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF363457; AAK60137.1; -.
EMBL; BC004692; AAH04692.1; -.
INTERPRO; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
PFam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDZ.
                                                         SEQUENCE OF 82-743 FROM N.A.
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655
986
743
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                                                                           TISSUE=Breast;
                                                                                                 Strausberg R.;
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Q9BXL7;
15-JUN-2002 (
15-JUN-2002 (
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Matches 234;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-hymus, spleen and liver. Also found in promyelocytic leukemia HL-hymboma Raji cells and colorectal adenocarcinoma SW480 cells. Unphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa S3, Wolt-4, A549 and G431 cells. Burkitt's SIMILARITY: CONTAINS I CARD DOMAIN.
SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
CAUTION: SUPPOSED to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21255663; PubMed-11356195; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                     Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;
"CARD11 and CARD14 are novel caspase recruitment domain
(CARD)/membrane-associated quanylate kinase (MAGUK) family members
that interact with Bcll0 and activate NF-kappaB.";
J. Biol. Chem. 276:11877-11882(2001).
                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        > L (IN REF. 2).
913A4B015D2B36CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.1%; Score 396.5; DB 1; 34.0%; Pred. No. 2.2e-14; ive 66; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG
PROSITE; PS50055; GUANYLATE_KINASE_2; FALSE_NEG
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUANYLATE KINASE.
 15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:16393; CARD11.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                     MEDLINE=21192234; PubMed=11278692;
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442
748
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                                                                                                                                                     SEQUENCE FROM N.A.
                                               CÁRD11 OR CÁRMA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interaction.
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123
673
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                                                                                                                   NCBI_TaxID=9606;
                                   Carma 1
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9

Gaps

23;

Matches 102; Conservative

Query Match Best Local Similarity

Length 1147; Indels

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Ducham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
A Clamp M., Smink L.J., Aliscough R., Almeida J.P., Babbage A.K.,
A Clamp W., Smink L.J., Aliscough R., Almeida J.P., Babbage A.K.,
Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
A Dhaml P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
A Barn P.D., Dockree C., Carfend D.V., Griffiths M.N.D., Hall C.,
A Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
A Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
A martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
A McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-21292987; PubMed-11259443; Wang L., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A., Meridan B., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A., Bertin J.; Merriam S., Glucksmann M.A., DiStefano P.S., Alnemri E.S., Bertin J.; "CARDIO is a novel caspase recruitment domain/membrane-associated guanylate kinase family member that interacts with Bcl10 and activates
                                                                                                                                                                                                360 TVMLQLEEVERERDQAFHSRDEAQTQYSQCLIEKDKYRKQIRELEEKNDEMYIEMVRREA 419
                                          LMNEVIKLQQQMKAKDLQRCELLARLRQLEDEKKQMTLTRVE-LLTFQERYYKMKEERDS 182
                                                                                    HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                       ---AEKDILE 163
                                                                                                                                                                                                                                                          QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFOKSKMACQLYREKVN 223
                                                                                                                                                                                                                                                                                                  300 HDRKEALEDROELVNRIYNLQEEARQAEELRDKYLEEKEDLELKCSTLGKDCEMYKHRMN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thome M., Tschopp J.;
Bcll0, induces Bcll0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                             224 ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       QEQSLRTASDQES -- GDEELNRLKEENEKLRSLTFSL -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaide O., Martinon F., Micheau O., Bonnet D., "Carmal, a CARD-containing binding partner of phosphorylation and NF-kappaB activation."; FBBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF-kappa B.";
J. Biol. Chem. 276:21405-21409(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21255663; PubMed=11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4AN STANDARD; PI
Q9UGR5; Q9UGR6; Q9Y3H0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3) (Carma 3).
CARD10 OR CARMA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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09BWT7; 09U
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us-09-767-215-2\_copy\_126\_420.rsp

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RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramesy Y., Rogers L., Ross M.T.,
Scott C.E., Sepra H.K., Skuce C.D., Smalley S., Smith M.L.,
Scott C.E., Sepra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Scott C.E., Williams S.A., Williamson H., Willey D.L.,
Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Kavasaki K., Sasaki T., Asakawa S., Rogers J., Shimizu N.,
RA Mincohima S., Kawasaki K., Yoshizaki T., Asakawa S., Roders J., Shimizu N.,
RA Shintani A., Shibuya K., Yoshizaki T., Asakawa S., Roder J., Shimizu N.,
RA Borman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang E., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang C., White J., Willingham D., Wu H., Yao Z.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Berdshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Wilson R.,
RA Mind K., Shikh T., Kurahashi H., Saitta S., Budarf M., Kedra D.,
RA McDermid H.E., Johnson L., Mandis E., Waterston R., Wilson R.,
RA Min U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Withinson P., Bodenteith A., Hartman R., Hu X., Khan A.S., Lane L.,
RA Wilkinson P., Bodenteith A., Hartman R., Hu X., Khan A.S., Lane L.,
RA Filann V. Wright H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "FUNCTION: Activates NF. kappaB via Bcll0 and IKK.
-!- FUNCTION: Activates NF. kappaB via Bcll0 and IKK.
-!- SUBUNT: CARD10 and Bcll0 bind to each other by CARD-CARD
INTERACTION: They both participate in a complex with MALT1, where
MALT1 binds to Bcll0 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUB SPECTIFICITY: Detected in adult heart, kidney and liver;
-!- Inver levels in intestine, placenta, muscle and lung. Also found
in fetal lung, liver and kidney.
-!- SIMILARITY: CONTAINS 1 CARD DOWAIN.
-!- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
-!- Like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: Ref.4 sequence differs from that shown due to various gene identification problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q -> R (IN REF. 4).
K -> KQ (IN REF. 4; CAB63075).
R -> L (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              > L (IN REF. 4).
8377319AB82A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL). POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 329.5; DB 1 Pred. No. 7.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The DNA sequence of human chromosome 22."; Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY032928; AAK54454.1; -...EMBL; AL049851; CAB63075.1; ALT_SEQ.EMBL; AL049851; CAB63076.1; ALT_SEQ.EMBL; AL022315; CAB42832.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.5%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim U.J., Shizuya H., S
Seroussi E., Fransson I
Wilkinson P., Bodenteic
Tilahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
917
932
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917 91
932 93
1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcllb-mediated NF-kappa B induction.";
J. Biol. Chem. 276:30589-30597(2001).
--- FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
--- SUBGUNIT: CARDIO and Bcll0 bind to each other by CARD-CARD interaction. They both participate in a complex with MALT1, where MALT1 binds to Bcll0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- TISSUE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
-:- SIMILARITY: CONTAINS I CARD DOMAIN.
-:- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
63 FHEVLRIKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                          QKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELT 268
                                                                                                                                                                                                                                ---LRRARGPPPGAEEKEKEKEKEKEPDNVDLVSELRAENQQLTASLRELQEGLQQEASR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       like domain. But none of these 3 domains are detected by PROSITE. Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21391892; PubMed=11387339; McAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Benito A., Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Bimpl, a MAGUK family member linking protein kinase c activation to Bcll0-mediated NF-kappa B induction.";
                      123 EQSLRTASDQESGDEELNRLKEENE-----KLRS----LTFSLAE-----
                                                                                                                                           -----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARD. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1021 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF363456; AAK60136.1; -. PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                    269 DOVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
450
565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 11
138 49
558 56
1021 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARDIO OR BIMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                             CARA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Bimpl)
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                                                                                                                                                                                                                                                                                                                                                                                                                               P58660;
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CARA_MOUSE
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Length 1021;

DB 1;

Score 322.5;

22.1%;

Query Match

g

δŏ

10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADH-----SRMKREVSAH 62

9

Gaps

49;

Indels

50; Mismatches 115;

Matches 100; Conservative

Best Local Similarity

.; 6

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                               9
                                                                                                                                                     ----LRRARGPPPGAEEKEREPDGADLLSELRAENQRLTASLQELQEGLQQEMSRPGAAG 306
                                                                                     62 HFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bertin J., Guo Y., Wang L., Silnivasula S.M., Jacobson M.D., Poyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E., Distefano P.S., Almemi E.S.; Du M.-Q., Dyer M.J.S., Robison R.E., Distefano P.S., Almemi E.S.; Du M.-Q., Dyer M.J.S., Robison R.E., Disterance a novel caspase recruitment domain-containing protein that interacts with Bc110/CLAP and activates NF-kappa B."; J. Blol. Chem. 275-141082-41086(2000) — 1- FUNCTION: Activates WF-kappaB via Bc110 (By similarity).

-1- FUNCTION: Activates WF-kappaB via Bc110 (By similarity).

-1- SUBUNT: Self-associates. CARD9 and Bc110 bind to each other by CARD-CARD interaction (By similarity).

-1- SUBCELULAR LOCATION: Cytoplasmic (By similarity).
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                               10 LQEELNQEKGQKEVLLRRCQQLQ-----EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                   ----KDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKM
                                                                                                                                                                                                                                                                                                 307 SERILLDILEHDWREAQDSROELCQKLHAVQGELQWAEELRDKYLQEMEDLRLKHRTLLK
                                                                                                                                                                                                                                                                                                                                      ACQLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCE
                                                                                                                                                                                                  122 QEQSLRTASDQESGDEE-----LINRLKEENEKLRSLTFSLAE------
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
6F33089CB7E6BAC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
          No. 1.7e-10;
smatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Caspase recruitment domain protein 9 (rCARD9)
CARD9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 AA
                               Mismatches
              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley;
MEDLINE-20576268; PubMed=11053425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARD.
31 1%; Pic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      LLTTVTSLEGTKAMLEAQLORT 448
                                                                                                                                                                                                                                                                                                                                                                                                      274 LRTQLRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF311288; AAG28791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001315; CARD.
PROSITE; PS50209; CARD; 1
                               Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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277
420
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536 AA;
              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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ISSOB-RELINDALSTORMS;
ISSOGAT T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
"Nibomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                              63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 VCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQL-----RQLQA 283
                                                                       Gaps
                                                                                                                                                                                                       112 ESGLTQLLMTEVMKLQKKVQDLTALLSSKDDFIKELRVKDSLLRKHQERVQRLKEECELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILNE-20576268; PubMed-11053425;
Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D.,
Bertin J., Guo Y., Wang L., Srinivasula S.M., Jacobson M.D.,
Boyet J.-L., Merriam S., Du M.-Q., Dyer M.J.S., Robison K.E.,
DiStefano P.S., Alnemri E.S.; Corruitment domain-containing protein that
"CARD9 is a novel caspase recruitment domain-containing protein that
interacts with Bc110/CLAP and activates NF-kappa B.";
J. Biol. Chem. 275:41082-41086(2000).
                                                                                                                                       17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS------RMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Activates NF-kappaB via Bcl10.
SUBUNIT: Self-associates. CARD9 and Bcl10 bind to each other by CARD-CARD interaction: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 HTLKLRHAMEORPSOELLWDLOOERDLLQARVOELEVSVOEGKLHRNSPYIQVLEEDWRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 EQ-SLRTASDQESGDEELNRLKEENE----KLRSLTFSLAEK-----DILEQSLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                   37;
   Length 536;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                   123;
Score 283.5; DB 1
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAR9_HUMAN STANDARD; PRT; 536 AA. 09H257; 09H854; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Caspase recruitment domain protein 9 (hCARD9)
                                                                   58; Mismatches
19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-492 FROM N.A. TISSUE=Muscle;
                                                                   Conservative
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--GRLKQQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 EPPGVLKQE 292
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                                                                   91;
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Query Match
Best Local S
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                                                                   Matches
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Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 EKGQKEVLLRRCQQLQEHL----GLAETRAEGLHQLEADHS------RMKREVSAH 62
TISSUE SPECIFICITY: Highly expressed in spleen. Also detected in liver, placenta, lung, peripheral blood leukocytes and in brain. SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N -> S (IN REF. 3).
LSSGEPPEKER -> PAGLPGIGAVC (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 FHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 SRELKRCKEENYDLAMRLAHQSEEKGAALMRNRDLQLEIDQLKHSLMKAE--DDCKVERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 EQ-SLRTASDQESGDEELNRLKEE----NEKLRSLTFSLAEK------DILEQSLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 HTLKLRHAMEQRPSQELLWELQOEKALLQARVQELEASVQEGKLDRSSPYIQVLEEDWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 VCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 536;
                                                                t
                                                            CAUTION: Ref. 2 sequence differs from that shown due frameshift in position 360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6EB1835315B83DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARD. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.2e-08
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(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.8%; Score 274.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                      EMBL; AF311287; AAG28790.1; -. EMBL; AK024001; BAB14766.1; ALT_FRAME. EMBL; BC008877; AAH08877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62267 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.48;
                                                                                                                                                                                                                                                                                                                                                  Genew, HGNC:16391, CARD9.
InterPro, IPR001315, CARD.
PROSITE, PS50209; CARD: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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277
419
12
492
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117 2
332 4
12
482 4
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRHY_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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      SO THE PRESENTATION OF THE
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-:- FUNCTION: INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLUED IN
                                                                                                                                                                                                                                                                                                                                                                                    -i-TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN THE FILIFORM PATILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
                                                                                                                                                                                                                                                                  ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM-BINDING DOMAINS. DOMAIN I CONTAINS TWO EF-HAND CALCIUW-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERRES OF PEPTIDE REDEATS OF VARYING REGULARITY. AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED BY IONIC INTERACTIONS. THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. THE MOLECULE. DOMAIN 9 CONTAINS IN THE MOLECULE. DOMAIN 9 CONTAINS IN THE MOLECULE. DOMAIN 9 CONTAINS IN THE WOLECULE. DOMAIN 9 CONTAINS IN THE WOLECULE. DOMAIN 9 CONTAINS IN THE WOLECULE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEELNQEKGQK----EVLLRRCQQLQEHLGLAETRAEGLHQL-----EADHSRMKRE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 S-100 LIKE.

33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).

183781 MW; AE17D2A159F12B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 LELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LVERIHSLR-----ERAVAAERQR-----EQYWEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 202.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
Probom; PD003407; CaBP_5100; 1.
PROSITE; P500018; EF_HAND; 1.
PROSITE; P500303; S100_CABP; 1.
Keratinization; Repeat; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P02633; 4ICB.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z19092; CAA79519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S28589; S28589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1407 AA;
                                                                                                                                                                                                                                                                                                                     DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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DOMAIN
NP_BIND
SEQUENCE
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Q9JLT0;
  PROSITE;
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                    Local
                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";

J. Cell Biol. 143:49-63(1998).

- FUNCTION: MINUS-END DIRECTED MICROTUBBLE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBGNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDSONE AT ANAPHASE, AND IS
QUANTITATIVELY DISCARDED THE NED OF THE CELL DIVISION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                         797 KLREEEQLLQEREEERLRRQERERKLREEEQLLQEREEERLRRQERERKLREEEQLLRQE 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93024922; PubMed-1406971;
Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
"CENP-E is a putative kinetochore motor that accumulates just before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.; Wiltotic HeLa cells contain a CENP-E-associated minus end-directed minus mater ".
                                                         -- OAYSARDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 247 OREISQSL -- VEKDSLRRQVFE -- LTDQVCELRTQLRQLQAEPPGVLKQE 292
                                                                                                                                                                                                 Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NAY-2000 (Rel. 39, Last annotation update)
Centromeric protein E (CENP-E protein).
                                                      EQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMARY; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
                                                                                                                                                                                                                                                                                                                                                               2663 AA
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE-95196755; PubMed-7889940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-98437347; PubMed-9763420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND/OR SPINDLE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 215005; CAA78727.1; -. PIR; S28261, S28261. HSSP; P17119; 3KAR. Genew; HGNC:1856; CENPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microtubule motor.";
EMBO J. 14:918-926(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 359:536-539(1992).
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (
01-JUL-1993 (
30-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 117143;
                                                                                                                                                                                                                                                                                                                                                               CENE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitosis.
                                                                                                                                                                                                                                                                                                        RESULT 9
CENE_HUMAN
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- CAPPING.

- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
CHAIN SUBUNITS (WHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.
- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
- SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                       SAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ATTQSNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE---AQK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELQEQSLRTASDQESGDEELNRLK-------EENEKLRSLTFSLAEKDILEQS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 LDEARGS------RQELVERIHSLRERAVAAERQREQYWEEKEQTLLOFQKSKMACQL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 YREKVNALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQ 277
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE-Brain;
MEDLINE=20483650; Pubmed=11027611;
Yam J.W.P., Chan K.W., Li N., Hsiao W.L.W.;
Molacular cloning and functional analysis of the promoter region of rat nonmuscle myosin heavy chain-B gene.";
Biochem. Biophys. Res. Commun. 276:1203-1209(2000).
-i- FUNCTION: CELLULAR WYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                              3 LAGAIGSLQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREV--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain, nontation myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                               SEELHIITSEKDKLFSEVVH-----KE---SRVQGLLEEIGKTKDDL------
                    Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                      81;
                                                                                                                                                                                           12.9%; Score 188.5; DB 1; Length 2663; 24.2%; Pred. No. 0.006;
                                                                                                                                                                                                                                        Indels
                                                                                                                            ATP (BY SIMILARITY).
W: CEFC13880C8C8CB8 CRC64;
                                                            KINESIN-MOTOR.
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                        Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1976 AA.
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                  312087 MW;
                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 LRQLQAEPPGVLKQEART 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRNALES ---- LKOHOET 979
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                        Cell cycle; Centromere.
DOMAIN 1 335
                                                               335
2471
2663
93
                                                                              336 247
2472 266
86 9
2663 AA;
                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      885 LLEEKNILAEQLQA-ETELFAEAEEMRARLAAKKQEL---EEILHDLESRVEGEEERNQI 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 EQYWEEKEQTLLQFQKSKMACQLYREKV-----NALQAQVCELQ---KERDQAYSA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 LKEENEKLRSLTFSLAEKDILEQSLDEARGSRQEL-----VERIHSLRERAVAAERQR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       772 AGVLAHLEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQRNC---AAYLK 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 LAE-----TRAEGLHQLEADHSRMKREVSAHFHEVLRLKD------EMLSLSLHYSN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 ALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQEQSLRTASDQESGDEELNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Plectin 1 (PLTN) (PCN) (300-KDa intermediate filament-associated protein) (IFAP300) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1976;
                                                                                                                                                                                                                                                                                                                                                                                                             70; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 RDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPPGVL 289
                                                                                                                                                                                                                                                                                                                                                Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 186.5; DB Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 4473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cricetulus griseus (Chinese hamster).
                                                                                                                                HSSP; PLUSOF, LENG.
INTERPRO; PLUSOF, LENG.
INTERPRO; IPR000409; Myosin_N.
INTERPRO; IPR002028; Myosin_Lail.
INTERPRO; IPR002018; Myosin_tail.
INTERPRO; IPR001019; Spectrin.
InterPro; IPR0011609; Myosin_head; Pfam; PF001615; IQ; I.
Pfam; PF001576; Myosin_Lail; I.
Pfam; PF02736; Myosin_Lail; I.
PRINTS; PR0010193; MYOSIN_RAIL
SMART; SM0001193; MYOSIN_head; I.
SMART; SM000115; IQ; I.
SMART; SM000145; MYOSIN_head; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228963 MW;
                                                                                                            EMBL; AF139055; AAF61445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.8%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Conservative
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1976
185
701
711
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                            HSSP; P10587; 1BR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLE1_CRIGR
Q9JI55;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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MADLINE-970212319; FULDMENG-0020314;

MADLINE-970212319; FULDMENG-0020314;

MADLINE-970212319; FULDMENG-0020314;

MADLIGATION OF PLECTIN AS A SUBSTRATE OF P34CdC2 kinase and applied of a single phosphorylation site.";

J. BIOL. CHEM. 271:8203-8208(1996).

C. I- FUNCTION: INTERLINES INTERMEDIATE FILAMENTS WITH MICROTUBULES AND MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDEANGOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABLILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT STABLILIZATION OF THEIR DYNAMICS.

C. I- SUBDINT: HOMODIMER OR HOMOTETRAMER.

C. I- DOMAIN: THE N-TERMINUS CAN BIND INTEGRIN BETA-4.

C. I- DOMAIN: THE N-TERMINUS CAN BIND INTEGRIN BETA-4.

C. I- PIM: PHOSPHORYLATED BY CDC2: REGULATES DISSOCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSIS.

C. I- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.

C. I- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
                                                                                                                                                                                                                                                         The 300-kDa intermediate filament-associated protein (IFAP300) is a
Chordata; Craniata; Vertebrata; Buteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                           MEDLINE=20334248; PubMed=10873583;
Clubb B.H., Chou Y.-H., Herrmann H., Svitkina T.M., Borisy G.G.,
Goldman R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROD DOMAIN
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CH 1.
CH 2.
SPECTRIN 1.
SPECTRIN 3.
SPECTRIN 3.
SPECTRIN 4.
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLOBULAR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00019; ACTININ.1; PARTIAL. PROSITE; PS00020; ACTININ.2; FALSE_NBG. PROSITE; PS50021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLECTIN 1.
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InterPro; IPR001715; Calponin-11ke.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR002017; Spectrin.
Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 20.
SMART; SM000350; Plect; 32.
SMART; SM00150; SPEC; 4.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96215219; PubMed=8626512;
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                                                                                                                                                                                                                                                                                            hamster plectin ortholog
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719
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     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q01082; 1BKR
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=10029;
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                                                                   Cricetulus.
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Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
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                                                                                                                                                                                                                                                                                                                                                                                 LEEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRL 2251
                                                                                                                                                                                                                                                                                                                                                                                                   70 KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                     125 -----SLRTAS---DQESGDEELNRLKEE----NEKLRSLTFSLAEKDILEQSLDEAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264
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                                                                                                                                                                                                                                                                            (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAEAERLKLRMAEMSRAQARAEEDAQRFRKQAEEIGEKLHRTELATQEKVTLVQTLEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 GSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC----QLYREKVNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- DQAYSARDSAQREISQSLVEKDSLRRQV
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                                                                                                                                                                                                                                                                                            4 X 4 AA TANDEM REPEATS OF G-S-R-X.
                                                                                                                                                                                                                                                                  PLECTIN 32.
BINDING TO INTERMEDIATE FILAMENTS
                                                                                                                                                                                                                                                                                                                               12.7%; Score 186; DB 1; Length 4473; 27.2%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                38; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY CDC2).
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                                  PLECTIN 6
PLECTIN 7
PLECTIN 8
PLECTIN 9
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3965
4003
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4094
4234
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3018
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es 87; Conserv
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SEQUENCE
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PLE1\_HUMAN STANDARD; PRT; 4684 AA. 015149; 016640; 015148; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)

DI AC I

RESULT 12 PLE1\_HUMAN

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The precting gene causes epidermolysis bullosa simplex with precting the causes because sepidermolysis bullosa simplex with precting and J. Pathol. 158:617-625(2001).

C. -! FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO CC. HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBRARE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE CC. -! SUBUNT: HOMODIMER OR HOMOTETRAMER.

C. -! ALTERNATIVE PRODUCTS: 3 ISOFOMAS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING; 1 (SHOWN HERE), 2 AND 3; ARE CC. -! ALTERNATIVE PRODUCTS: 3 ISOFOMAS; 1 (SHOWN HERE), 2 AND 3; ARE CC. -! ALTERNATIVE PRODUCTS: 3 ISOFOMAS; 1 (SHOWN HERE), 2 AND 3; ARE CC. -! ALTERNATIVE PRODUCTS: 3 ISOFOMAS; 1 (SHOWN HERE), 2 AND 3; ARE CC. -! ALTERNATIVE PRODUCTS: 3 ISOFOMAS; 1 (SHOWN HERE), 2 AND 3; ARE CC. -! DOMAIN: THE N-TERMING INTERACTS WITH ACTIN, THE C-TERMINUS MITH CC. -! DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE N-TERMINUS INTERACTS WITH ACTIN, THE N-TERMINUS CC. -! DOMAIN: THE N-TERMINUS CAN BIND INTERSITUS, LAMIN B; WHEREAS BOTH THE N-TERMINUS CAN BIND INTERSITUS, ENTERSATION FROM WITH MUSCULAR DYSTROPHY (MD-EBS OR EB-MD), AN AUTOSOMAL RECESSIVE CC. -! DISEASE: DEFECTS IN PLECI ARE THE CAUSE OF EPIDERMOLYSIS BULLOSA WITH MUSCULAR DYSTROPHY (MD-EBS OR EB-MD), AN AUTOSOMAL RECESSIVE CC. -! SIMILARITY: CONTAINS 3 PLECTRIN REPEATS.

C. -! SIMILARITY: CONTAINS 3 PLECTRIN REPEATS.

C. -! SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.

C. -! SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96312447; PubMed-8698233;
McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg B.L., Lane B.B.,
Bullzich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H., Hachisuka H., Nishikawa T., McLean W.H.I., Uitto J.; "Homozygous deletion mutations in the plectin gene (PLEC1) in patients with epidermolysis bullosa simplex associated with late-onset muscular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiche G., Uitto J., Hintner H.; "A compound heterozygous one amino-acid insertion/nonsense mutation in the plectin gene causes epidermolysis bullosa simplex with plectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
                                                                      Euteleostomi;
                                                                                                                                                                                                                                      Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.; "Human plectin: organization of the gene, sequence analysis, and chromosome localization (8q24)."; Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VATIANT MD-EBS LEU-429 INS.
MEDLINE=21090821; PubMed=11159198;
Bauer J.W., Rouan F., Kofler B., Rezniczek G.A., Kornacker I.,
Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
                                                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              (ISOFORMS 2 AND 3), AND DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97049959; Pubmed=8894687;
                                                                                                                                                                                                                  MEDLINE=96210632; PubMed=8633055;
                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes Dev. 10:1724-1735(1996).
                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA cloning and
                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                           TISSUE-Placenta;
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SIMILARITY).

WAGNIMPRODLRATYOUREECOWVAKUDREPRSLHPHVP
GUTULOWRAMASLRARGLVRETFAWCHFFWYLTNEGIAHL
ROYLHLPPETVAASLGRVRREVAMVHPARFFPHVOAVOGPL
GSPPKRGPLPTEGORLYRRELEEVSPETPVVPATTORTLA
RPGPEPAPAT -> MSCEDAEVRAVSEDVSNGSSGSFSBGD
TLPWMLGKTORSRSGGGAGSNGSVLDPAERAVIRIA (IN
ISOFORM 2 AND ISOFORM 3).
L -> LL (IN MD-EBS).
L -> LL (IN MD-EBS).
FTIG-VAR_011336
MISSING (IN MD-EBS).
FTIG-VAR_011336
MISSING (IN MD-EBS).
FTIG-VAR_011337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQEL--QRANMVSSCELELQEQ--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Gaps
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                                 4 X 4 AA TÂNDEM REPEATS OF G-S-R-X.
PHOSPHORYLATION (BY CDC2) (BY
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Best Local Similarity
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                   Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding; Phosphorylation; Alternative splicing; Epidermolysis bullosa; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                             GLOBULAR 1.
CENTRAL FIBROUS ROD DOMAIN.
GLOBULAR 2.
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InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR003205; S10_plectin.
InterPro; IPR00307; CH; 2.
Pfam; PF00507; CH; 2.
Pfam; PF00501; S10_plectin; 1.
SMART; SM00130; CH; 2.
SMART; SM00150; SPEC; 3.
SMART; SM00150; SPEC; 3.
FROSITE; PS000109; ACTININ_1; FALSE_NEG.
PROSITE; PS000109; ACTININ_1; FALSE_NEG.
PROSITE; PS000101; CH; 2.
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EMBL; U53204; AAB05427.1; --
EMBL; U636.0; AAB05428.1; --
EMBL; U636.09; AAB05428.1; --
EMBL; V37003; CAA65765.1; --
HSSP; Q01082; IBKR.
Genew; HGNC:9069; PLECI.
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                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY IN VIVO.
SUBUNT: HOMOIDIMER (PROBABLE).
TISSUE SPECIFICITY A MAJOR SIGNAL WAS OBSERVED IN TESTIS AND BRAIN, BUT IT WAS ALSO DETECTED IN THYMUS, SPLEEN, KIDNEY, HEART
                                                                                                                                                                                                                                                                                                                                  Madaule P., Furuyashiki T., Reid T., Ishizaki T., Watanabe G., Morii N., Narumiya S.;
"A novel partner for the GTP-bound forms of rho and rac.";
FEBS Lett. 377:243-248(1995).
-:- FUNCTION: PUTATIVE RHO/FAC EFFECTOR THAT BINDS TO THE GTP-BOUND FORMS OF RHO AND RACI. IT PROBABLY BINDS P21 WITH A TIGHTER
                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citron protein (Rho-interacting, serine/threonine kinase 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 185; DB 1; Length 1597; Pred. No. 0.0055;
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MW; 7B7286C2305676DA CRC64;
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COLLED COIL (POTENTIAL).
RHO/RAC BINDING.
POLY-LYS.
                                                                                                               1597 AA
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SMART; SM00233; PH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                           2691 EARRRQHEAEEGVRRKQEELQQLEQQ 2716
          261 -- RRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00130; DAG_PE-bind; 1. Pfam; PF00130; DAG_PE-bind; 1. Pfam; PF00169; PH; 1. SMART; SM00109; Cl; 1. SMART; SM00109; Cl; 1.
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26.5%;
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                                                                                                         CTRO_MOUSE
P49025;
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Best Local Similarity

Query Match

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                                                             388 QEEMISELROOKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKSRLLELETRLREVSLE 447
                                                                                                                                                         117 CELELQEQSLRTASDQ------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                                                                  EEQVLDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQSRARADQRI 665
 92; Gaps
                                QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Citron protein (Rho-interacting, serine/threonine kinase 21)
 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1286 AA
 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                   251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Connell M., Goela D., Harper M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTRO_HUMAN STANDARD;
014578; Q9UP27;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC002563; AAB71327.1; -. EMBL; AB023166; BAA76793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 347-1286 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR STK21 OR KIAA0949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:1985; CIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
CTRO_HUMAN
                                11
                                                                                            62
                                                                                                                          448
                                                                                                                                                                                                                                                       557
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EMBL;
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Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                    ----LDEASGANDEIVQLRSEVDHLRREIT----EREMQLTSQKQTM---EALKTTCTML 296
                                                                                                                                                                                                                                                                                                                           62 HFHEVLRLKDEMLSLSLHYSNALQEKE----LAASRCRSLQEELYLLKQELQRANMVSS 116
                                                                                                                                                                                                                                                                                                                                       297 EEQVMDLEALNDELLEKERQWEAWRSVLGDEKSOFECRVRELQRMLDTEKQSRARADQRI 356
                                                                                                                                                                                                                                                                                                       79 QEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLREVSLE 138
                                                                                                                                                                                                                                                                                                                                                                 117 CELELQEQSLRTASDQ-------ESGDEELNRLKEENEKLRSLTFSLAEKDI 161
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                    11 QEELNQE-KGQKEVLLRRCQQLQEHLGLAETRAEGL-HQLEADHSRM-----KREVS-A 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-ocr-2001 (Rel. 40, Last sequence update)
Lecor-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                               162 LEQSLDEARGSRQELVE---RIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SVCELQKERDQAYSARDSAQREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Obara M., Ishiguro N., Shinagawa M.;
"Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                             12.5%; Score 183; DB 1; Length 1286; 26.2%; Pred. No. 0.0057;
                                                                                                                                                                                     PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                98; Indels
                                                                                                                                                                                                                 17 SH3-BINDING (POTENTIAL).
146506 MW; 498101F79EA75E85 CRC64;
                                                                                                                                                        COILED COIL (POTENTIAL). RHO/RAC BINDING. POLY-LYS.
                                            Pfam: PF00130; DAG_PE-bind; 1.
Pfam: PF00180; PH; 1.
Pfam: PF00180; CNH; 1.
SMART; SM00109; C1: 1.
SMART; SM00036; CNH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
Coiled coil; Phorbol-ester binding; SH3-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1976 AA
                                                                                                                                                                                                                                                     26.2%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 SQSLVEKDSLRRQVFELTDQVCELRTQLRQLQ 282
MIM; 605629; -
InterPro; IPR001180; Citron.
InterPro; IPR002219; DAG_PE-bind
InterPro; IPR001849; PH.
InterPro; IPR000861; REM_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                         558
561
512
670
822
1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos
                                                                                                                                                                                                                           1286 AA;
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYHA_BOVIN
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                             Query Match
                                                                                                                                              NON_TER
DOMAIN
                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYHA_BOVIN
                                                                                                                                                                                                                                                                  Matches
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THE MOST OF THE RESIDENCE OF THE STATE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-s1b.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      864 VKEKOTKVEGELEEMERKHOOLLEEKNILAEOLOAETELFAEAEEMRARLAAKKOELEEI 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRLKDEMLSLSLHYSNALQ-EKELAASRCRSLQEEL---YLLKQELQRANWVSSCELELQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924 LHDLESRVEEEEERNQILQNEKKKMQAHIQDLEEQLDEEEGARQKLQLEKVTAEAKIKKM 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQSLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQEELNQEKGOKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSA---HFHEV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.4%; Score 182; DB 1; Length 1976; 22.1%; Pred. No. 0.0099; tive 78; Mismatches 130; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 LRERAVAAERQREQYWEEK-----EQTLLQFQKSKMACQLYREK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
MW, 614435451C0F790 CRC64;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coiled coil; Alkylation; Multigene family.

DOMAIN 1 785 MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; IQ_region.
InterPro; IPR000099; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
Prom; PP00063; myosin_head.
Pfam; PP00612; IQ; 1.
                                                                                                                                                         IISSUE=Brain cortex;
MEDLINE=95301542; PubMed=7782316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB022023; BAA36494.1; -.
                                                                                                      SEQUENCE OF 204-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U15716; AAA87715.1; -. HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00242; MYSc; 1.
                                                                                                                                                                                                                                                     Itoh K., Adelstein R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00015; IQ;
SMART; SM00242; MYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
SEQUENCE
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NP_BIND
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Oggye6 mus musculu O88317 mus musculu Q21022 caenorhabdi

29u0s7 mytilus

Q9xvh4 caenorhabdi

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

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Q8txi4 methanopyru O9bw73 xenopus lae O14812 homo sapien O60588 homo sapien O99450 homo sapien O96055 homo sapien O96075 homo sapien O96075 homo sapien O96073 homo sapien O96393 mus musculu O99mb9 mus musculu O63731 rattus norv O63731 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O15738 dictyosteli
Q21025 caenorhabdi
O30Kt9 leishmania
O73732 xenopus lae
Q912u8 mus musculu
042263 xenopus lae
Q25142 halocynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |::::||: :|::||: |: |: |: |: || | | | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LAGAIGSLOEELNQEKGQKEVLLRRCQQLQ-EHLGLAETRAEGLHQLEADHSRMKREVSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%; Score 396.5; DB 4; Length 34.0%; Pred. No. 3.9e-14; Live 66; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1
SEQUENCE 1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL: AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
FLJ00120 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1171 AA
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                       090XE6
088317
0208317
0208317
08TXI4
08TXI4
08TXI4
080588
090588
090588
0904450
0904450
0904450
090415
090713
0903731
025561
025714
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0811D2
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0811D2
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042263
025142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                               876
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224442
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1041
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1099
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1098
1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=SPLEEN;
  Best Local Sim
Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TES3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TES3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
  Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  075033 homo sapien
Q14981 homo sapien
Q44980 homo sapien
Q94935 mus musculu
Q9v587 drosophila
Q61043 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O8r443 rattus norv
O96jv2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8tes3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9vje5 drosophila
O44929 drosophila
                                                                                                                                                                                  (without alignments)
1321.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        January 22, 2003, 08:49:36; Search time 45.9946 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                1 ECLAGAIGSLQEELNQEKGQ......TQLRQLQAEPPGVLKQEART
                     5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                               671580 segs, 206047115 residues
                       GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                      US-09-767-215-2_COPY_126_420
1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TES3
Q8R443
Q96JV2
O75033
Q14981
Q14980
Q9D935
Q70365
Q9V587
Q61043
Q6VJES
                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_vertebrate:*
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sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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8: sp_organe
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Match 1
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9

Gaps

23;

QEQSLRTASDQES--GDEELNRLKEENEKLRSLTFSL-------AEKDILE 163 

122

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Q9uqq7 homo sapien O95287 homo sapien Q8tba6 homo sapien Q9u0s5 mytilus gal homo sapien homo sapien

Q9UQQ7 Q95287 Q8TBA6 Q9UQS5

396.5 198.5 196.1 196.1 194.1 193.5 193.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5 191.5

Score

Result Ş Ş g

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Eukaryota; Metazoa;
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075033
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2005, clone PLACE4000009, weakly similar to myosin heavy chain, nonmuscle type B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ELNRLKEENEKLRSLTFSLAEK-DILEQSLDEARGSRQELVERIHS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 -RSRLEVAEVNGRLAELSLHMKEEKCOWSKERTGLLQSMEAE-----KDKILKLSAEIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --QEELYLLKQELQRANMVSSCEL------ELQE----QSLRTASDQESGDE-- 137
                                                                                                                                          384 TVMLQLEEVERERDQAFHSRDEAQTQYSQCLIEKDKYRKQIRELEEKNDEMRIEWVRREA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LQEELNQEKGQKEVLLR-----TRA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 REQEKLLGQLKEFQADKEQSEAELQTVREENCHLNTELQEAKGRQEEQGAQVQRLKDKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LRERAVAAE------RQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 ELQK----ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAEPP
                         QSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVN
                                                     EGLHQLEADHSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSL----
                                                                                                                 ALQAQVCELQKERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%; Score 198.5; DB 11; Length 691; 23.7%; Pred. No. 0.0015; tive 64; Mismatches 119; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=OFA-SD; TISSUE=CEREBELLUM; Vie-Luton M.-P., Francon J.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY078385; AAL85572.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35572.1; -. 77276 MW; E4FF5AA1784377FE CRC64;
                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                         691
                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, KIAA1536 protein.
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                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVL----KQEAR 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q96JV2;
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Matches
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129 ASDQESGDEELNRIKEENEKLRSLTFSLAEK-----DILEQSLDEARGSRQELVERIHS 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRE--RAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCELELQ-EQSLRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN:
MEDITE=981NE)
SSK1 N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 EEALVHV-----RKEEKEAVSAR-RALENEL-----EAAQGNLSQTTQEQKQLSEKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LQEELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAHFHEVLRL
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                                                                                                                                                   TISSUE-PLACENTA;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Akamanta A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027863; BAB55415.1;
Interpro: IPR002928; Myosin_tail.
Frank PF01576; Myosin_tail.
SEQUENCE 612 AA; 72111 MW; EEOEACB9710B594E CRC64;
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel¢
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                      Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 196; DB 4; Length 61 ilarity 25.8%; Pred. No. 0.0018; Conservative 62; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00DC42FDE419EED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 SARDSAQREISQSLVE-----KDSLRRQVFELTDQVCELRTQLRQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 TKRQLLEQTLKDLEYELEAKSHLKDDRSRLVKQMEDKVSQLEMELEE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 15, Last annotation update)
KIAAQ445 protein (D377C10.5) (KIAA0445).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1313 AA
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148254 MW;
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EMBL; AL049569; CAB96825.1;
SEQUENCE 1313 AA; 148254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n human brain.";
Res. 4:345-349(1997).
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Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
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                                                                                                                          SEQUENCE FROM N.A.
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                                                                NCBI_TaxID=9606;
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586 ATAAE-EREASLRERDAALKQLE----ALEKEKAAKLEI----LQQQLQVANEARDSA 634
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                                                                                                                                                                                                    PRT; 2115 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Biol. 116:1303-1317(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=94013066; PubMed=8408288;
                                            247 QREISQSLVEKDSLRRQVFEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 26.6%
les 93; Conservative
                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                   NuMA protein.
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Q9D935;
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Q9D935
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                                            12;
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                                                                                                                                                                                                                                                                                                AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                       412 VLOLETLKQEAATLAANNTQLQARVEMLETERGQGEAKLLAERGHFEEEKQQLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                 98 QEELYLLKQELQR--ANMVSSCELELQEQSLRTASDQESGDEELNRLKEENEKLRSLTFS 155
                                                                                                                              210 EALEGSLFEVOROLAQLEARREQLEAEGOALLLAKETLTGELAGLROQIIATQEKASLDK 269
                                              Gaps
                                                                                         ----- QEHLGL-A 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||||| ::: :|::||:|| || || ::
---RSTVNALTSELRDLRAQRESAAAHAQEVRRLQEQARDLGKQRDSCLREAE----
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                                                                                                                                                                             ETRAEGLHQLEAD-HSRMKREVSAHFHEVLRLKDEMLSLSLHYSNALQEKELAASRCRSL
                                                                                                                                                                                                                                                                                                                                                        156 LAEKDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 QLYREKVNALQAQVCELQKERDQAYSARDSAQREISQSL----VEKDSLRRQVFELTDQV
                                                                                                                                                                                                                                                                                                                                                                                                  371 ESEKTALSEKL---MGTR-----HSLATISLEMERQKRDAQSRQEQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NUMA protein.
NUMA protein.
Eukarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 FHEVLRLKDEMLSLS------LHYSNALQEKELAASRCRSLQEELYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-92176238; PubMed-1541636;

Compton D.A., Szilak I., Cleveland D.W.;

Compton D.A., Szilak I., Cleveland D.W.;

"Primary Structure of NuMA, an Intranuclear protein that defines Novel Pathway for Segregation of Proteins at Mitosis.";

J. Cell Biol. 116:1395-1408(1992).

EMBL; Z11584; CAA776701.1; -.

SEQUENCE 2101 AA; 236297 MW; 2097F679D4E38E69 CRC64;
                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104; Indels 104;
Length 1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 194; DB 4; Length 2101; 26.6%; Pred. No. 0.008;
                                            Indels
  DB 4;
                                          56; Mismatches 102;
                                                                                      1 ECLAGAIGSLQEELNQEKGQKEVLLRRCQQL-------
13.4%; Score 195.5; DB 25.9%; Pred. No. 0.0042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ELRTQLRLLEDARDGLRRE 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 CELRTQLRQLQAEPPGVLKQ 291
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
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                                            Matches
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Yang C.H., Lambie E.J., Snyder M.;
"NuMA: an unusually long coiled-coil related protein in the mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: || | :|: | | 412 VLQLETLKQGEARLLAERGLESEERQQLSSLITDL 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 -----LKQELQRANMVSSCELELQEQSLRT-----ASDQESGDEELNRLKEE--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRER 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 KQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQK---EQQLKEV-AEKQEATRQDHA-QQL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 AVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQEELN---QEK----GQKEVLLRRCQQLQEHLGLAETRAEGLHQLEADHSRMKREVSAH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maekawa T., Kuriyama R.; "Primimary Structure and microtubule-interacting domain of the SP-H antigen: a mitotic map located at the spindle pole characterized as homologous protein to NuMA."
J. Cell Sci. 105:589-600(1993).
EMBL: 21583: CAA77669.1; ---
HSSP; P80220; IDIP.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 194; DB 4; Length 2115; 26.6%; Pred. No. 0.0081; Live 49; Mismatches 104; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QREISQSLVEKDSLRRQVFEL-------TDQVCELRTQLRQLQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 124 0 -> P (IN REF. 2).
1587 1587 Q -> H (IN REF. 2).
2115 AA; 238274 MW; DA5686215054DBEE CRC64;
                                   -----TDQVCELRTQLRQLQ
                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                            REQUENCE FROM N.A.

SEQUENCE FROM N.A.

RAIN=C57BL/6J; TISSUE=PANCREAS;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Yamanaka I.,

Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A listorman W., Gasakeri T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Watsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Radota K., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Radi K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Radi K., Soffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruyons P., Marchionni L., Mashima J., Hume D.A., Kamiya M., Lee N.H.,

Rusaki H., Toyo-Oka K., Schoenbach C., Sakamoto N.,

Radota K., Sato K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Radota K., Rawaij H., Royo-Oka K., Wang K.H., Weltz C., Kawaji H., Kohtsuki S.,

Radota K., Radota K., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVCELQK----ERDQAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LONGLDESQQERNDLMQLKLQLEDQVTELRSRVQELEAALATARQEHSELTEQYKGLSRS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 :| : : : | : | : | : | : | 10 HG--ELSEERDILSQQQGDHVARILELEDDIQTM----SDKVLMKEVELDRVRDTVKALT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 REQEKLLROLKEFQADKEQSEAELQTVREENCCLNTELEEAKSR---QEEQGAQVQRLKD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ELNRLKEENEKLRSLTFSLAEK-DILEQSLDEARGSRQELVER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LH--RSRLEVAEVNGRLAELSLHMKEEKCQWSKERTGLLQSMEAE-----KDKILKLSA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEELYLLKQ------ELQRANMVSSC-ELELQEQSLRTASDQESGDE----- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LQEELNQEKGQKEVLLR-----TRA 42
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AKO07393; BAB25009.1;
MGD; MGI:1914738; 1810009B06Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 193.5; DB 11; Length 691; 22.9%; Pred. No. 0.0028; Live 66; Mismatches 116; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77280 MW; 4759E5478839D9B7 CRC64;
                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2238 AA.
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    Created)
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22.9%; Pi
O1-JUN-2001 (TrEMBLrel. 17, C1
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2001 (TrEMBLrel. 17, La
1810009806Rik protein.
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                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                691 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 86; Conserv
                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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ID 070365
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SL-AEKD-----ILEQSLDEARGSRQE----LVERIHSL-RERAVAAERQREQYWEE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LHYSN-ALQEKELA---ASRCRSLQEEL------YL-LKQELQRA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 NMVSSCELELQEQSLRTASD---QESGDE-----EL----NRLKEENEKLRSLTF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---HEVLRLKDEMLSLS-- 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 SLQEELNQEKGQ-----KEVLLRRCQ-----QLQEHLGLAETRAEGLHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
STRAIN-BALB/C; TISSUE-BRAIN;
STRAIN-BALB/C; TISSUE-BRAIN;
Towanyko M.M., Murali R., Greene M.I., Marks M.S.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF051357; AAC05573.2; -..
SEQUENCE 2238 AA; 257562 MW; 494EA2C111F0165B CRC64;
                                                                                                                                                                   Craniata; Vertebrata; Euteleostomı;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murali
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUB=BRAIN;
COWAN D.A., GAY D., Beiler B.M., Zhao H., Yoshino A., Davis J.G.
TOMAYKO M.M., Murali R., Greene M.I., Marks M.S.;
"Characterization of mouse tGolgin-1 (golgin-245/ trans golgin-Characterization of mouse tGolgin-1 (golgin-245/ trans golgin-230/256kD golgin) and its upregulation during oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%; Score 193.5; DB 11; Length 2238; 24.9%; Pred. No. 0.0091; ive 59; Mismatches 121; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=BRAIN;
Gay D., Beiler B.M., Zhao H., Bhandoola A., Tomayko M.M., J.
Marks M.S., Greene M.L.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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                          (TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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  Created)
                                                                                      Golgi autoantigen golgin subtype a4.
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.2%;
Best Local Similarity 24.9%;
Matches 100; Conservative 5
(TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Cell Biol. 0:0-0(2002).
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                                                                                                                                              Mus musculus (Mouse).
01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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Q9V587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                    11;
                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : | 1: DWESTKQRIARLELENERLKHDLERSQTTFGRTTMTTSQELDRAQERADKASAELRRTQA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVLRLKDEMLSLSLHYSNALQEKELAASRCRSLQEELYLLKQELQRANMVSSCE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1456 AA; 164239 MW; 49E04C6716443ECA CRC64;
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 192; DB 5; 25.1%; Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003833; AAF58930.1; -.
FlyBase; FBgn0033420; CG1931.
InterPro; IPR000533; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00194; TROPOMYOSIN,
                CG1931 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1671 VQTSTLVSSLEAELSRIKLQTHVMEQENLLLKDELERLKQLHRCPDLSDLQQKMSSVLSY 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1780 KSQLAVSQAKVQDLEDVLQNVNLQMAEIESDLQVTRQEKEAVKQEVMSLHRQLQNAIDKD 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 RMKREVSAHFHEVLRLKDEMLSLSLHYSNAL-QEKELAASRCRSLQEELYLLKQEL---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 -LQFQKSKMACQLYREKVNALQAQVCELQKERDQAYSARDSAQREIS-----QSLVEKD 258
                                                                                                                                ----TASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQEL-----V 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AIGSLQ-EELNQEKGQKEVLLRRCQQLQEHLGLAETRAEGL------HQLEADHS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belkaid Y., Milon G., Crocker P.R.; "Molecular characterisation of ninein, a new coiled-coil protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                             333 ELRVTQSDAERAREEAAALQEKLEKSQGEVYRLKAK--LENAQGEQESLRQELEKAQSGV
                                                                                                   ERIHSLRERAVAAERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCELQKERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 NEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRERAVAAERQREQYWEEKEQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bouckson-Castaing V., Moudjou M., Ferguson D.J.P., Mucklow M., Belkaid Y., Milon G., Crocker P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                      238 QAYSARDSAQREISQSLVEKDSLRRQVFELTDQVCELRTQLRQLQAE 284
                                                                                                                                                                                                                                      441 HLQDKLDKACTENRRLVLEKEKLTYDYDNLQSQLDKALGQAARMQKE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249168 MW; FDB8EC0F240E58E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 -QRANMVSSCELELQEQSLRT-ASDQES--GDEELNRLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1840 ----WVSETAPHLSGLRGQQRRLSWDKLDHLMNEEPQLLCQESK 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 SLRRQVFELTDQVCELRTQLRQ-----LQAEPPGVLKQEAR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 192; DB 11; 24.4%; Pred. No. 0.011; tive 68; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VJE5;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:105108; Nin.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Cell Sci. 108:0-0(1996).
EMBL; U40342; AAA83234.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the centrosome."
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                  Q61043
Q61043;
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                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                    RESULT 10
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RX ARAIN-BERKELEY;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Il P.W., Hoskins R.A., Calle R.F.
RA Adamstides D.G., Scherer S.E., Il P.W., Hoskins R.A., Calle R.F.
RA George R.A., Lewis S.E., Richards S., Amburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yadadell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andraws-Pfannkoch C.R., Baldwin D.,
RA Ballew R.W., Benos P.V., Berman B.P., Bandario C.R., Malklos G.L.G.,
RA Abril J.F., Benos P.V., Berman B.P., Bandario D., Botahakov S.,
RA Borkova D., Botcher M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botcher A., Deng Z., Marsakararoglu L., Beasley E.M.,
RA Cherry J.M., Cawley S., Dablke C., Davenport L.B., Davies P.,
RA Glodek A., Gody E.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Glodek A., Gody F., Gorrell J.H., Gu Z., Galbart W.M., Classer R.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Adalai M., Ralush F., Rapen G.H., Ke Z., Guan P., Harris M.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Woy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Marlson D.R., Marltman G.S., Pan S., Pollard J., Puri, Wang X.,
RA Shue B.C., Siden-Kiamos I. Simpson M., Stuonskin M.P., Smith H.O.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stuong S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Wolder J.C., Shap G. S., Pollar S., Polla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 GALQEEIAKLQEKMTIQQKEVESRIAEQLEEEQRLRENVKYLNEQIATLQSELVSKDEAL 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 DSLESERVNKTDECEILQTEVRMRDEQIRELNQQLDEVTTQLNVQKADSSALDDMLRLQK 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LGLAETRAEGLHQ----LEADHSRMKREVSAHFH------EVLRLKDEML----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D6F7916A9C532F16 CRC64;
  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 191.5; DB 5; 23.7%; Pred. No. 0.0088; ive 69; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SLSLHYSNALQEKELAASRCRSLQEELYLLKQEL-----
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                                                                                       Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02; CAP_GLY; 2.
1690 AA; 189063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0020503; CLIP-190.
InterPro; IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003655; AAF53604.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CLIP-190 protein.
CLIP-190 OR CG5020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01302;
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Matches 101;
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEQLOQQÀAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTQSNLEAKSKQLEA-ANG 896
                                                                                                                                                                                    724 QIQLEKESIEQQLALKQNELEDFQKKQSESEVHLQEIKAQNTQKDFELVESGESLKKLQQ 783
                                                                                                                                                                                                                                                      -----ERAVAA----ERQREQYWEEKEQTLLQFQKSKMACQLYREKVNALQAQVCE 231
----QRANMVSSCELEL----QEQSLRTASDQESGDEELNRLKE--ENEKL-RSLTFSL-- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 SGDEELNRLKEENEK----LRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLRERAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAERQ-----REQYWEEKEQTLLQFQKSKMACQLYREKVNA------RE
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                                          664 EGTEEKSTLLEKTEKELVQSKEQAAKTLNDKEQLEKQISDLKQLAEQEKLVREMTENAIN
                                                                                                                                                                                                                                                                                                 LQKERDQAYSARDSAQREISQSLVEKDSLRRQV----FELTDQVCELRTQLRQLQAEPPG
                                                                                                                            ----EARGSRQ--ELVERIHSLR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Last sequence update) U-JUN-2001 (TrEMBLrel. 17, Last annotation update) Microtuble binding protein D-CLIP-190. CG5020.
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Pred. No. 0.0088;
1; Mismatches 119;
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J. Cell Biol. 0:0-0(1998).
ENBL; AF041382; AAB96783.1; -.
FlyBase; FB90000053; CLIP-190.
InterPro; IPR000938; CAP-Gly.
Pfam; PF01102; CAP-Gly.
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21.48; Pred
tive 71; 1
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Best Local Similarity 21.4%
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                                                                                                                                   ---AEKDILEQSLD----
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                                                                                                                                                                                              MEDLINE=99115642; PubMed=9915833;
Bascom R.A., Srinivasan S., Nussbaum R.L.;
"Identification and characterization of golgin-84, a novel Golgi integral membrane protein with a cytoplasmic coiled-coil domain.";
J. Biol. Chem. 274:2923-2962(1999).
EMBL; AF085199; AAD09753.1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                               ; Score 191; DB 4; Length 73:
; Pred. No. 0.0041;
43; Mismatches 122; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023021; AAH23021.1; -.
SEQUENCE 731 AA; 82976 MW; 6661F19BA16425B0 CRC64;
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82990 MW; E708D023C60B02BA CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Golgi autoantigen, golgin subfamily a, 5.
Homo sapiens (Human).
                    Last sequence update)
Last annotation update)
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     Created)
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                                                                       Homó sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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26.5%;
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Best Local Similarity 26.5%
Matches 86; Conservative
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TISSUE=PLACENTA;
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                                                                                                                                                                                   TISSUE=TESTIS;
                                                        Golgin-84.
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                                         125 SLRTASDQESGDEELNRLKEENEKLRSLTFSLAEKDILEQSLDEARGSRQELVERIHSLR 184
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    KDSLRRQ------VFELTDQVCELRTQLRQLQAE------PPGV
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Best Local Similarity 26.5%; Pred. No. 0.0033;
Matches 86; Conservative 43; Mismatches 122; Indels
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; AJ132949; CAB36967.1; -.
SEQUENCE 585 AA; 66384 MW; FEEAF1F35F551681 CRC64;
                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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                                                                                        LKQEAR 294
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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"CAMP- and cGMP-dependent protein kinase
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/note= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation
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e= "Peroxisomal targetting signal"
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96..799
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.e= "RGD cell attachment sequence"
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/note= "7
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/note= "Casein Kinase II phosphorylation site"
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'note= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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ce= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Protein Kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e- "Protein Kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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ce= "Tyrosine kinase phosphorylation site"
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ce= "Casein kinase II phosphorylation
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e= "Casein kinase II phosphorylation
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e= "Leucine zipper pattern"
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e= "N-myristoylation site"
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589..592
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.e= "N-myristoylation site"
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                                                                            The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., anaemia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crobn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                  Score 467; DB 22;
Pred. No. 2.2e-51;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by TGG"
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                                                 Claim 1; Fig 1A-1E; 109pp; English
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                                                                                                                                                                                                                                                                                                                                                                                   Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                 1004 AA;
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                                                                                       The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimulates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for It is also useful for the treatment of autoimmune disorders (e.g., aystemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders (e.g., amemaia, myelodysplastic syndromes), myocardial infarctions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
apoptosis; hyperproliferative disorder; autoimmune; neurological;
inflammatory disorder; viral infection; stress-related response.
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                                                                                                                                                                                                                                                                                                                                         100.0%; Score 467; DB 22; Length 1139; 100.0%; Pred. No. 2.6e-51; Live 0; Mismatches 0; Indels 0;
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/note= "Protein kinase C phosphorylation site"
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168..171
175..183
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/note= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human caspase recruitment domain, CARD-11 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG
                                                                Disclosure; Fig 2A-2C; 109pp; English.
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/note= "Protein kinase C phosphorylation site"

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/note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
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te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                note= "Protein kinase C phosphorylation site" 71..474
note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                  .08.510
'note= "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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Moote= "Casein kinase II phosphorylation site"

61..766
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te= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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ce= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                           "Protein kinase C phosphorylation site"
                 "Casein kinase II phosphorylation site"
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"Tyrosine kinase phosphorylation site"
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:e- "Glycosaminoglycan attachment site"
                                                                                                                                         ..381
te= "Casein kinase II phosphorylation
                                                                         "Protein kinase C phosphorylation
                         .195
e= "Tyrosine kinase phosphorylation
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te= "N-myristoylation site"
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:e= "N-glycosylation site"
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..e= "SH3 domain"
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634.
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787..789
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508..51
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638..64
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The present sequence represents novel human caspase recruitment
domain, CARD-11. The polynucleotide encoding this sequence was
isolated from a human T-cell DONA library. Also described are
novel human sequences for CARD-9 and CARD-10 (AAU01205, AAU01206)
and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact
with Bol-10 which is thought to activate nuclear factor (NF) kappaB
cond apoptosis. The sequences of the invention can be used for
treating a disorder associated with abnormal levels of apoptosis by
modulating the expression or activity of CARD-9, CARD-10, or CARD-11.
They can be used for the treatment of hyperproliferative disorders
(e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),
neurological disorders (e.g. Alzheimer's disease), inflammatory disorders
(e.g. cronn's disease), and viral infection (e.g. HIV). The CARD
polypeptide, polynucleotide and an antibody which selectively binds to
CARD can be used in screening and detection assays (e.g. chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
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335..937
Anote= "Protein Kinase C phosphorylation site"
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.120..1123
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                           "Casein kinase II phosphorylation site"
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1050..1055
/note= "N-myristoylation site"
1088..1091
                                                                                   "Casein kinase II phosphorylation site"
                                                                                                                                                   372..875
/note= "Casein kinase II phosphorylation
882..1147
/note= "Guanylate kinase (GUK) domain"
897..900
                                                                                                                           .859
e= "Protein kinase C phosphorylation
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.e= "Casein kinase II phosphorylation
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e= "N-myristoylation site"
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2000US-0685791.
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2000US-0507533.
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10-OCT-2000;
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18-FEB-2000;
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                  The
mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy, treatment and prophylaxis). The Modulate it. CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation. cancer, NF *RappaB signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
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                                                                                                                                                         Length 1147;
                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                           Score 139; DB 22;
Pred. No. 1.3e-08;
                                                                                                                                             29 8%; Scor.
36.5%; Pred. No. 1...
''e 17; Mismatches
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                                                                                                                                                                                                                                                                                                       726 KEEAHWTIQRCSGPVTLHYKVNHEG 750
                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                  ABB64619 standard; Protein; 1445
                                                                                                                                                                                                                                                                                     69 LEEAVGLLRRVDGFCCLSVKVNTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
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2000US-0614150
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                                                                                                                                                                                        31; Conservative
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                                                                                                                           1147 AA;
                                                                                                                                                                          Local Similarity
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11-JUL-2000;
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                                                                                                                                                                     409 ISFOKEGSV-GIRLIGGNEAGIFVTAVOPGSPASLOGLMPGDKILKVN-----DMDM 459
                                                            Gaps
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                                                                                                               64
                                                                                                                  LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVL
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   Length 1445;
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DB 22;
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Score 85.5; DB Pred. No. 0.16;
                                                      11; Mismatches
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18.3%;
33.8%;
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11-JUL-2000; 2000US-0614150
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genes from Drosophila and
                                                         Conservative
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nes 20; Conserv
                           Local Similarity
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   Query Match
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Isogai T,
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17-FEB-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                       Homo sapiens
                                                                                                                                                                                      18-OCT-1999;
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                   13-NOV-2001
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Kodama T,
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AAM93968;
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AAB93753
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                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 25059
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llarity 31.2%; Pred. No. 0.28;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                         EW.
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                                                                      ABB66089 standard; Protein; 1916 AA
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                Drosophila melanogaster.
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Matches 20; Conserv
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                      1564 ISKL 1567
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     76 LRRV 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stomach cancer-associated genes, useful as markers in blood tests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K, Yamamoto J;
Otsuki T, Aburatani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 548;
                                                                                    stomach cancer; marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                         Human stomach cancer expressed polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for screening for the early stages of the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 22;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:13422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 67-69; 242pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
Midorikawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB93753 standard; Protein; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.18;
34.48;
                                                                                                                                                                                                                                                                                                                                                                    99JP-0300253.
99US-0159590.
2000JP-0118776.
2000UP-018332.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000WO-JP05063
                                                                                                                                                                                                                                                                                                                                                   99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                               peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-570287/64.
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les 21; Conserv
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Human; kinase; enzyme; PKIN-13 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charch-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarchoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-2001; 2001WO-US27219
 16-JUL-2002 (first entry)
                         Human PKIN-13 protein.
                                                                                                                                                                                                                                                                                                                                                                                              WO200218557-A2.
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2000;
29-SEP-2000;
06-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002
                                                                                                                                                                                        Domain
                                                                                                                                                                                                                    Jomain
                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                               Jomain
                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                             Кеу
 polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence, at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length converse are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length converse are also useful for the cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13642 represent human cDNA sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                 Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 548;
                                                                                                                                                                                                                               Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 13422; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                          Nagai K,
                                                                                                                                                                                                                              Isogai T, Nishikawa T, Hayashi K,
, Sugiyama T, Wakamatsu A, Nagai K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 2
Pred. No. 0.22;
9; Mismatches
                                                                                                                                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                         02-MAY-2000; 2000JP-0183767.
                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                    99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.4
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the present invention.
                                                                                                                                                                                                    (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                       WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA;
                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
              sapiens
                                     EP1074617-A2
                                                                                                                                               11-JAN-2000;
                                                                                                                    29-JUL-1999;
                                                                                                                                    27-AUG-1999;
                                                                07-FEB-2001
                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
              Ношо
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"Leucine zipper domain"

..754

/note= 733..75 /note= 2000US-234902P. 2000US-236499P. 2000US-238389P. 2000US-240542P.

2000US-231357P. 2000US-232654P.

2000US-229873P

"GLGF domain"

/note= "G 391..471 .439

"PDZ domain" "PDZ domain"

/note=

"GLGF domain" Location/Qualifiers

"PDZ domain" "PDZ domain"

/note= /note=

.101

.280 .469

/note=

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The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcor.Marie-Tooth disease or seizures), call proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                               New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as
                                                                       Gandhi AR
                                                                    Walia NK, Hafalia AJA, Yao MG, Gandhi AR
Patterson C, Yue H, Baughn MR, Tribouley
'S, Lu Y, Ison CH, Au-Young J, Tang YT;
'M Marcus G, Zingler KA, Lu DAM, Lal PG;
', Kearney L, Policky JL, Thangavelu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 68; Page 174-176; 218pp; English.
(INCY-) INCYTE GENOMICS INC.
                                                                                                         ?, _Ding L, Pat
Elliott VS,
Burrill JD, M
Warren BA, K
                                                                       Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukemia or lymphoma)
                                                                                                                                                                                                                                                                                                                             WPI; 2002-329769/36.
                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD34310
                                                                                                                                           Thornton M,
Azimzai Y, B
Ramkumar J,
                                                                                                         Gururajan R,
                                                                       Bandman O,
                                                                                                                                                                                                                                                         Burford N;
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ij

8; Gaps

23; Indels

34.48;

ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75 

r 76 L 75

92 75

рp ò g

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AAE21718 standard; Protein; 928 AA.

RESULT AAE2171 AAE21718;

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but was obtained in electronic format directly from WIPO
  specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200244340-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fang YT, Go
Yamazaki V,
                                                                                                                                                                                                                                                                                            30-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2002.
                                                                                                                                                                                   L 558
                                                                                                                                                           76 L 76
                                                                                                                                                                                                                                                                    ABG66725;
                                       Sequence
                                                                Query Match
                                                                                                                                                                                   558
                                                                                      Matches
                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                    ABG66725
                                                                                                                                                                                                                                                g
                                                                                                                                                             ŏλ
                                                                                                                                                                                  q
   SSXS
                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a fock supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappositics, forensics, gene mapping, identification of mutations in the printed diagnostics amino acid sequences of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed
                                                               ;
                                                                                                        16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                               8;
                                       DB 23; Length 928;
                                        Score 80; DB 2:
Pred. No. 0.45;
                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 52725; 103pp; English.
                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #22357.
                                                                                                                                                                                                                        ABG22366 standard; Protein; 1037 AA.
                                        17.18;
34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                        (first entry)
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS86553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                928 AA;
                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                        18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                           Ma.
Local St..
21;
                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001.
                                                                                                                                                              455 L 455
                                                                                                                                      76 L 76
                                                                                                                                                                                                                                                ABG22366;
                 Sequence
                                        Query Match
                                                                Matches
                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                               ABG22366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfasion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, sarkinson's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                                                                                                                                                                                                                       16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid disorders, cancer and promoting wound healing -
                                                       Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J,
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V,
                                                                                                                  23;
                                                          DB 22;
                                                                                        Pred. No. 0.52
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 629-632; 672pp; English.
                                                             Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Zhou
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG66725 standard; Protein; 1651 AA.
                                                          17.18;
34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2001; 2001WO-US47004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel polypeptide #60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000; 2000US-0028952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RW,
ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-508509/54.
N-PSDB; ABK94949.
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V, Ujwal 1
1037 AA;
                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection
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              regeneration of bone, cartilage, tendon, ligament and/or never tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmuno disorders e.g. multiple sclerosis and myasthenia quavis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsorlatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; cogqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antianaemic; gene therapy; cancer; proliferative disorder; hypertension; meurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinutia; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                        QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA
  disorders and platelet disorders such as thrombocytopenia,
                                                                                                                                                                                                                                                                                                    Length 1651;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.
                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                    DB 23;
                                                                                                                                                                                                                                                                                                  17.0%; Score 79.5; D 34.6%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB42658 standard; Protein; 1675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|| : |:|| |
645 VEILRN-NTHLALTVKTN 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                          Query Match 17.0%
Best Local Similarity 34.6%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                                                                                                                                            1651 AA;
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                                                                                                                                                                                                                                                            Sequence
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                                                                                               AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthitic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; confishosition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat capress.
                                                                                                                                                                                                                                                                                                                        proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinfiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QISVIGGNLT -- GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
   ×
   reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1675;
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                 useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; betal-syntrophin; SNT B1; PDZ domain; GLGF loop;
Novel nucleic acids and peptides derived from open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.0%; Score 79.5; Di
34.6%; Pred. No. 1.2;
tive 12; Mismatches
                                                                    Claim 11; Page 4028-4032; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hasegawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB21149 standard; peptide; 538 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHF domain; muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goedert M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2000; 2000WO-GB00374.
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668 VEILRN-NTHLALTVKTN 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-558226/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1675 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                            The present sequence is the protein sequence of human betal-syntrophin. It is described with reference to the methods of the invention, which involve the identification of compounds which are able to modulate the interaction between PDZ domains (also known as DHF or GLGF domains) and protein kinases. The invention also comprises peptide fragments derived from stress-activated protein kinases which are involved in protein phosphorylation. The compounds and peptides can be used in the treatment of muscular diseases, for example muscular dystrophy, or in cases where modulation of phosphorylation of proteins with PDZ domains or modulation of signalling via activin receptors or voltage gated channels is necessary, or in instances where the localisation of SARK3 at the neuromuscular junction or sarcolemma needs to be disrupted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of human beta2-syntrophin. It is described with reference to the methods of the invention, which involve the identification of compounds which are able to modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel methods for identifying compounds useful for treating muscular dystrophy comprising identifying modulators of protein kinase and {
m PDZ}
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Novel methods for identifying compounds useful for treating muscular dystrophy comprising identifying modulators of protein kinase and PDZ domain binding -
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            8 QGDALLEQ-----ISVIGG--NLTGIFIHRVTPGSAADQ-MALRPGTQIVMVDYEASEP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas
                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                          Length 538;
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                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an; beta2-syntrophin; SNT B2; PDZ domain; GLGF loop; domain; muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                          16.0%; Score 74.5; DB 21; 35.6%; Pred. No. 1.1; ive 10; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasegawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 -- GADLRDATHDEAVQALKRAGKEVLLEVK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 LFKAVLEDTTLEEAVGLLRRVDGFCCLSVK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 12c; 102pp; English.
                                                                                   Disclosure; Fig 12b; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB21150 standard; peptide; 540 AA
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A;
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Best Local Similarity 35.6%
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                             538 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21150;
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DHF dom
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been stolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                     ë,
interaction between PDZ domains (also known as DHF or GLGF domains) and protein kinases. The invention also comprises peptide fragments derived from stress-activated protein kinases which are involved in protein phosphorylation. The compounds and peptides can be used in the treatment of muscular diseases, for example muscular dystrophy, or in cases where medulation of phosphorylation of proteins with PDZ domains or modulation of signalling via activin receptors or voltage gated channels is necessary, or in instances where the localisation of SAPK3 at the neuromuscular junction or sarcolemma needs to be disrupted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                    16 ISVIGG--NLTGIFIHRVTPGSAADQ-MALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
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                                                                                                                                                                                                    Length 540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jai T, Hayashi K, Ishii S, Kawa
Nagai K, Kojima S, Otsuki T,
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                     Score 73.5; Di
Pred. No. 1.5;
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM93296 standard; Protein; 304
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                                                                                                                                                                                                     15.7%;
36.8%;
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2000JP-0118774.
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Best Local Similarity 36.89
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                              73 VGLLRRVDGFCCLSVK 88
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                                                                                                                                                                        540 AA;
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11-JAN-2000;
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specification, but was obtained in CD-ROM format directly from EPO.

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                                                                                       Ouery Match 15.6%; Score 73; DB 22; Length 304; Best Local Similarity 31.2%; Pred. No. 0.77; Matches 24; Conservative 14; Mismatches 25; Indels 14; Gaps
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286 EAVAILKRTKGTVTLMV 302
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Search completed: January 22, 2003, 08:52:19 Job time: 21.125 secs

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APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 2, An Sequence 31, An Sequence 31, Sequence 52, Sequence 52, Sequence 5, An Sequence 34, Sequence 15, Sequence 15, Sequence 15, Sequence 2, An Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SVIGG-----NLTGIFIHRY-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.6%; Score 73; DB 4; Length 2037; Best Local Similarity 31.2%; Pred. No. 1.4; Matches 24; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bartel, Paul L.

APPLICANT: Tavtigian, Sean V.

TITLE OF INVENTION: MASC2- An MMAC1 Interacting Protein

FILE REFERENCE: MASC2

CURRENT APPLICATION NUMBER: US/09/306,998

CURRENT FILING DATE: 1999-05-07

EARLIER APPLICATION NUMBER: US 60/084,740

EARLIER FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 2337

TYPE: PRT
US-09-562-737-26
US-09-091-405-2
US-09-100-804-31
US-08-545-860D-52
PCT - US94-600-52
US-08-545-04496-52
US-08-990-379-5
US-08-990-379-5
US-08-447-411-76
US-08-662-227-34
US-09-376-338-15
US-09-376-338-15
US-09-376-338-15
US-09-376-338-15
US-09-413-814-83
US-09-413-814-83
US-08-413-814-83
US-08-413-814-83
US-08-413-814-83
US-08-413-814-83
US-08-413-814-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-306-998-3; Sequence 3, Application US/09306998; Patent No. 6291173
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Patent No. 5821075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2019 EAVAILKRTKGTVTLMV 2035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-306-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-08-596-291-3
   qq
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Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Applisequence 16, Applisequence 16, Applisequence 2, Applisequence 3, Applisequence 31, Applisequence 20, Applisequence 20, Applisequence 14, Ap
                                                                                                                                                                                                                                               (without alignments)
429.229 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                            January 22, 2003, 08:52:30; Search time 6.375 Seconds
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Sequence 2
Sequence 2
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgg_2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/Re_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-306-998-3
US-08-106-291-3
US-09-080-855-12
US-09-290-640-46
US-09-290-640-46
US-09-290-640-46
US-09-100-804-16
US-08-023-454A-2
US-08-923-454A-2
US-08-923-454A-3
US-08-923-454A-3
US-08-923-454A-3
US-08-923-454A-3
US-08-923-454A-3
US-08-923-454A-3
US-09-108-271A-11
US-09-173-281B-20
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US-09-017-947-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                    US-09-767-215-2_COPY_568_660
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Minimum DB Maximum DB

Database

Result No.

Searched:

3;

Gaps

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TELECOMMUNICATION INFORMATION
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.4%
Best Local Similarity 28.9%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-100-804-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-080-855-12
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CONRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1071 EITLVNLKKDAKYGLGFQIIGGEKMETDLGIFISSVAPGGPADFHGCLKPGDRLISVNSV 1130
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                                                                                                COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-AUG-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1131 SLEGVSHHAAIEILQNAPEDVTL 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09100804 Patent No. 6066472 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 -----YEASEPLFKAVLEDITL 69
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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MASSACHUSETTS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
OPERATING SYSTEM: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-596-291-3
BOSTON
MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-09-100-804-3
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
APPLICANT: Hallman, Ulf
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
TILE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
FILE REFERENCE: L0461/7030
CURRENT APPLICATION NUMBER: US/09/080,855A
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: 08/805,583
EARLIER FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2466
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15.3%; Score 71.5; Di
Best Local Similarity 28.6%; Pred. No. 2.9;
Matches 24; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 72; DB 328.9%; Pred. No. 2.5; Live 15; Mismatches
PRICRATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER:: 31,616
                                                                                                                                                                                                                                                                                       LO461/7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-080-855-12; Sequence 12, Application US/09080855A; Patent No. 6083721
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NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
                                                                                        ; ORGANISM: Homo sapiens US-09-290-640-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Matches 25; Conserv
                                                                                                                                                   Query Match
Best Local Similarity
Matches 24; Conserv
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                 SOFTWARE: Pater
SEQ ID NO 46
LENGTH: 2485
TYPE: PRT
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Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
                                                                                                                                                                                                                          PRIMARY STRUCTURE AND FUNCTIONAL
EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-5EP-1933
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: LO461/7000W
TELECHONE: 617/720-3500
TELEPHONE: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
                                                                                      Sequence 2, Application PC/TUS9409943 GENERAL INFORMATION:
1131 VSLEGVSHHAAIEILQNAPEDVTL 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1131 VSLEGVSHHAAIEILQNAPEDVTL 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                        TITLE OF INVENTION: PRIMARY STR
TITLE OF INVENTION: TYROSINE PH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERITIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 28.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-290-640-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-09943-2
                                                                      PCT-US94-09943-2
                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                           APPLICANT:
                                                                                                                                APPLICANT
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                                                       RESULT 5
셤
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                                                                                                                                           1090 EITLYNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVAPGGPADLDGCLKPGDRLISVNS 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                       1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                   15;
     DB 4; Length 2485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.2%; Score 71; DB 4; Length 1881; 32.5%; Pred. No. 2.3; tive 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bartel, Paul L.
APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MASCI - An MMACI Interacting Protein
FILE REFERENCE: MMSCI Gene
CURRENT PELLING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: US 60/071,861
EARLIER APPLICATION NUMBER: US 60/071,861
SEARLIER PLING DATE: 1998-01-20
NUMBER OF SEO, ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
15.3%; Score 71.5; Di
28.6%; Pred. No. 2.9;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09100804
Patent No. 6066472
GENERAL INFORMATION:
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: GLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCT!
TITLE OF INVENTION: TYROSINE PHOSP!
                                                                                                                                                                                                                                                              1150 VSLEGVSHHAAIEILQNAPEDVTL 1173
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09233086 Patent No. 6337192
                                                                                                                                                                                                               53 ----YEASEPLFKAVLEDITL
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                                                      Conservative
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CORRESPONDENCE ADDRESS:
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Query Match 14.2%; Score 66.5; DB 3; Length 173; Best Local Similarity 33.3%; Pred. No. 0.31; Matches 16; Conservative 11; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08739485
Patent No. 586398
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
AFTILE OF INVENTION: NOVEL HUMAN LIM PROTEINS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                          OPERATING SYSTEM: DOS
SOFTWARE: FASESEO VERSION 1.5
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: BAUMENSTEATION NUMBER: 33,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/739,485
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COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,48°
FILING DATE:
CLASCATE
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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ORIGINAL SOURCE:
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ANTI-SENSE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LGFQ------IIGGEKMGRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLEG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Rowne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMITHKLINE Becham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-40G-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 13,616
RECISTRATION NUMBER: 13,616
RECISTRATION NUMBER: CA461/7003
TELEPHONE: 611-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LO461/7003
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 30.49
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-720-2441
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
        MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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US-09-100-804-16
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                               COUNTRY:
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Length 458;
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                                                                                                                                                                                                                                                       25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL
                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                  11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                         Query Match
14.2%; Score 66.5; DE
Best Local Similarity 33.3%; Pred. No. 1.3;
Matches 16; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66.5; Di
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FSASLSO VESTON 1.5
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/08923454A Patent No. 6004794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P50547
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REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: PSC
TELECOMMUNICATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 25:
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Creasy, Caretha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 amino acids
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                                                                                            FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King of Prussia
                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
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    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COM OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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ORIGINAL SOURCE:
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  STRANDEDNESS:
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                                                                                                                                     US-08-923-454A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH:
                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                            20 GGNLTG-----IFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.2%; Score 66.5; DB 2; Length 316; Best Local Similarity 32.5%; Pred. No. 0.74; Matches 27; Conservative 12; Mismatches 35; Indels 9
                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE MORRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CHITY: King of Prussia
REFERENCE/DOCKET NUMBER: PF-0142 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSBO Version 1.5
SURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08923454A Patent No. 6004794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFTCATION: 435
CLASSIFTCATION DATA:
PRIOR APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 VGLLRRVD-GFCCL-SVKVNTDG 93
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74 HQLCLKIDRGETHLWSPQVSEDG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                          INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: E
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
                                                                                                                                                                                          TOPOLOGY: linear
HAMBDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
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OPERATING SYSTEM:
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19406
8 PF
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STATE: PA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-923-454A-8
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Sequence 11, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                   TITLE OF
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       Gaps
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       3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: ||:| || || : |||| || : || || 390 GVLIHKVILGSPAHRAGLRPGDVILAIGEQMVQNAEDVYEAVRTQSQL 437
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       18; Indels
                                        25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                               5: SmithKline Beecham Corporation 709 Swedeland Road
       11; Mismatches
                                                                                                                                                                                                                                                                                        APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
CORRESPONDENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 Xaa = Arg or Cys
278 Xaa = Ala or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
                                                                                                                                                            Sequence 31, Application US/08923454A patent No. 6004794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P50547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 0435
PRIOR APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: BAUMEISTER, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET UNMBER: P5054
TELECOMMUNICATION:
                                                                                                                                                                                                                  Creasy, Caretha
Livi, George
Karran, Eric
Clinkenbeard, Helen
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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Best Local Similarity 33.3%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acid
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090
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CORIGINAL SOURCE:
US-08-923-454A-31
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US-09-008-271A-11
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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         16;
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         Matches
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WARREN, PATRICK V.
FONTION: METHODS FOR IDENTIFYINGHERBICIDAL AGENTS THAT INHIBIT DI PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%; Pred. No. 1.3;
Matches 16; Conservative 11; Mismatches 18;
                                                                                                         Tang, Tom Y.
Shah, Purvi
INVENTION: HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                             Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: SINIUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mohan-Peterson, Sheela
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08759581B Patent No. 5876945 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHISHOLM, DEXTER A.
APPLICANT: DINER, BRUCE A.
APPLICANT: DINER, BRUCE A.
APPLICANT: DONDADSON, GAIL K.
APPLICANT: JORDAN, DOUGLAS B.
APPLICANT: TANG, XIAO-SONG
APPLICANT: TROST, JEFFREY T.
APPLICANT: WANG, SHAOJIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 458 amino acids TYPE: amino acid
                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharm
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                       NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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APPLICANT:
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Best Local Similarity 24.7%; Pred. No. 1.9;
Matches 18; Conservative 16; Mismatches 25; Indels
NUMBER OF SEQUENCES: 29

CORRESPONDENCE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: 10898
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WINDOWS 3.1
SOFTWARTON NUMBER: US/08/759,581B
FILING DATE:
CLASSIFICATION INPORMATION:
NAMME: FLOOD, LINDA MAREH
SALEDHONE: 302-892-8112
TELECPAN: 302-892-8112
TELECPAN: 302-892-8112
TELECPAN: 302-892-8112
TELECPAN: 302-892-8112
TELECPAN: 302-892-8112
TELECPAN: SOFTWARE
STRANDEDENESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PROCEIN
ORIGINAL SORUKE:
STRAIN: SPINACH DI PROTEASE PROTEIN
US-08-759-581B-20
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: || :|| || 287 IYEAANILQGPDG 299

9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68

69 LEEAVGLLRRVDG 81 δy

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Search completed: January 22, 2003, 08:57:37 Job time : 8.375 secs

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Sequence 3,

Sequence 60, Appl Sequence 119, App Sequence 2, Appli Sequence 22, Appl Sequence 24, Appl Sequence 26, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32, Appl Sequence 33, Appl Sequence 60, Appl Sequence 60, Appl Sequence 805, Appl

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1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR FILING DATE: 2000-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-767-215-5
Sequence 5, Application US/09767215
Patent No. US2002008163641
GENERAL INFORMATION:
APPLICANT: BETLIN, John
TITLE OF INVENTION:
TITLE OF INVENTION:
FROTEIN FAMILY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 467; DB 10;
100.0%; Pred. No. 5.9e-48;
tive 0; Mismatches 0;
10 US-09-909-005-3

10 US-09-739-907-60

10 US-09-739-907-119

9 US-09-963-959-2

10 US-09-771-730-22

10 US-09-771-730-22

10 US-09-771-730-32

10 US-09-771-730-32

10 US-09-771-730-32

10 US-09-771-730-32

10 US-09-771-730-36

10 US-09-771-730-36

10 US-09-771-730-36

10 US-09-771-730-36

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10 US-09-771-730-36

10 US-09-78-60-5674

10 US-09-78-60-5674

10 US-09-78-61-805

10 US-09-81-805

10 US-09-81-81-1917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
     TYPE: PRT
ORGANISM: Homo sapiens
US-09-767-215-2
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     US-09-767-215-2
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60.5
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Best Local 9
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Matches
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Sequence 16, App
Sequence 964, App
Sequence 5, Appli
Sequence 1108, Ap
Sequence 2, Appli
Sequence 57, Appli
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Sequence 5, Appli
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                                                                                                                                                      (without alignments) 500.428 Million cell updates/sec
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                                                                                                                                January 22, 2003, 08:49:35; Search time 3.75 Seconds
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                     GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-911-826A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Query Match
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Sequence 14, Application US/10032159A

Patent No. US20020164703A1

GENERAL INFORMATION:

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: BUNCORING NUCLEIC ACIDS, AND METHODS OF USE

FILE REFERENCE: P.LJ 5100

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: US 60/257,457

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. US20020164703A1
Patent No. US20020164703A1
Patent No. US20020164703A1
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
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                                                                                                                                                                                                                                                                               Length 1138;
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                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 467; DB 10; Best Local Similarity 100.0%; Pred. No. 7e-48; Matches 93; Conservative 0; Mismatches 0;
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16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
FRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
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Matches 30; Conservative
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CRCANISM: Homo sapiens
US-09-767-215-5
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US-10-032-159A-14
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LENGTH: 113
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Sequence 11, Application US/09963959
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Sequence 11, Application US/09063959
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/963,959
CURRENT PILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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APPLICANT: Bartel, Paul L.
APPLICANT: Tartigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
CURRENT APPLICATION NUMBER: US/09/951,402
CURRENT FILIG DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
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35.2%; Pred. No. 0.014;
live 10; Mismatches 19;
                                                                                                                                                                                                                                                                                   Query Match 28.5%; Score 133; DB 9; I
Best Local Similarity 36.6%; Pred. No. 1.1e-07;
Matches 30; Conservative 16; Mismatches 36;
CURRENT APPLICATION NUMBER: US/10/032,159A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: US 60/257,457 PRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 37 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 80
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ORGANISM: Homo sapiens
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Matches 25; Conserv
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US-09-802-669-46
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US-09-998-425-3
                                                                                                                                                                                                                   Matches
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Best Local Similarity 31.2%; Pred. No. 3.3;
Matches 24; Conservative 14; Mismatches 25; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SVIGG----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                                                                                                        17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVWVDYEASEPLFKAVLEDTTLE 70
                                                                                                                                                                                                                                     Query Match 15.6%; Score 73; DB 9; Length 2037; Best Local Similarity 31.2%; Pred. No. 3.3; Matches 24; Conservative 14; Mismatches 25; Indels 14;
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APPLICANT: Bartel, Paul L.
APPLICANT: Tartiglan, Sean V.
APPLICANT: Tartiglan, Sean V.
TITLE OF INVENTION: MMSC2 - An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
CURRENT PAPLICATION NUMBER: US/09/951,401
CURRENT FILING DATE: 1201-09-14
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 3
LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
CURRENT APPLICATION NUMBER: US/09/922,101
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 60/084,740
PRIOR FILING DATE: 1998-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09951401 Patent No. US20020115104A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-922-101-3
; Sequence 3, Application US/09922101
; Patent No. US20020146711A1
; GENERAL INFORMATION:
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                                                             NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
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                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-402-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-401-3
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
APPLICANT: Watt, Jacqueline
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: 158H-345
CURRENT FILING DATE: 2001-03-09
PRIOR PLICATION NUMBER: US 09/665,615
PRIOR PLICATION NUMBER: US 09/665,615
PRIOR PLING DATE: 1999-04-12
NUMBER OF SED ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                            17 SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
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Publication No. US20030008346A1
Publication No. US20030008346A1
Publication No. US20030008346A1
APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Myriad Genetics, Inc.
ITLE OF INVENTIONS MASC1 - An MMAC1 Interacting Protein
FILE REFERENCE: MMSC1 Gene
CURRENT APPLICATION NUMBER: US/09/998,425
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/233,086
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
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                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                    DB 10;
3.3;
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ilarity 31.2%; Pred. No. 3.3;
Conservative 14; Mismatches
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Best Local Similarity 28.6%
Matches 24; Conservative
                              Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      71 EAVGLLRRVDGFCCLSV 87
; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patentin Ver. 2.0;

; SEQ ID NO 3

LENOTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                      ; ORGANISM: Homo sapiens US-09-922-101-3
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Best Local Similarity
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72 AVGLL 76
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US-09-764-868-964
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                           LOCATION:
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APPLICANT: Rotin, Daniela and Pham, Nam
APPLICANT: Rotin, Daniela and Pham, Nam
TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Methods of Use
FILE REPERENCE: DDW-5001-US
CURRENT APPLICATION NUMBER: US/09/911,826A
CURRENT FILING DATE: 2002-02-26
PRIOR PLILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 2,259,830
PRIOR APPLICATION NUMBER: 2,259,830
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                  Gaps
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/071,861; PRIOR FILING DATE: 1998-01-20; NUMBER OF SEQ ID NOS: 65; SOFTWARE: Patentin Ver. 2.0; SOFTWARE: Patentin Ver. 2.0; Type: PRIOR 3; Type: PRIOR 3; ORGANISM: Homo sapiens US-09-998-425-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 948, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APLICART: Rosen et al.
; TILLE OF INVENTON: NUMBER: US/09/764,868
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT PILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper software: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
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41.2%; Pred: No. 0.087;
"wiematches 13;
                                                                                                                                                                                               15.2%; Score 71; DB
ilarity 32.5%; Pred. No. 5.1;
Conservative 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 65
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ORGANISM: Homo sapiens
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US-09-911-826A-20
                                                                                                                                                                                                                  Local Similarity
hes 25, Conserv
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US-09-764-868-948
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Sequence 16, Application US/09911826A

Sequence 16, Application US/09/011826A

TITLE OF INVENTION: Reached and Pham, Nam

TITLE OF INVENTION: Methods of USe

FILE REFERENCE: DNA-5001-US

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: PCT/CA00/00042

PRIOR PAPLICATION NUMBER: PCT/CA00/00042

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16
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                                                                                                          NAME/KEY: SITE
LOCATION: (149)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (157)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                           NAME/KEY: SITE LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 964, Application US/09764868

Patent No. US2002016811131

GENERAL INFORMATION:

APPLICAT: Rosen et al.

TITLE OF INVENTYON: NUMBER: US/09/764,868

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT APPLICATION OF SEC 101.01-77

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEC 1D NOS: 1510

SOFTWARE: Patentin Ver. 2.0

SEC 1D NO 964
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                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIV 49
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                                                                                                                                                                                                                                                   29;
                                                                                                                        Query Match 14.7%; Score 68.5; DB 9; Length 163; Best Local Similarity 29.2%; Pred. No. 0.43; Matches 31; Conservative 16; Mismatches 30; Indels 29
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Best Local Similarity 32.5%; Pred. No. 1.8;
Matches 27; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                       92 RGDQLLSVN-----GVSVEGEQHEKAVELLKAAQG----SVKL 125
                                                                                                                                                                                                                                                                                                                         44 PGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10126099
Patent No. US20020170079A1
GENERAL INFORMATION:
APPLICANT: Goll, Surya K.
Hillman, Jennifer L.
Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN LIM PROTEINS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,099
FILING DATE: 18 APr-2002
CLASSIFICATION: CUNROWN>
PRIOR APPLICATION NUMBER: US/09/206,645
FILING DATE: CUNROWN>
APPLICATION NUMBER: US/08/739,485
FILING DATE: CUNROWN>
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
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; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-126-099-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 316 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-10-126-099-5
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Gaps

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20 GGNLTG-----IFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                   Search completed: January 22, 2003, 08:52:53
Job time : 5.75 secs
                                                  73 VGLLRRVD-GFCCL-SVKVNTDG 93
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                               - protein search, using sw model
                                                                               OM protein
                                                                                                                      Run on:
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January 22, 2003, 08:49:35 ; Search time 7.125 Seconds (without alignments) 1254.807 Million cell updates/sec US-09-767-215-2\_COPY\_568\_660 Title: Perfect score:

1 QVTMLAFQGDALLEQISVIG.....GLLRRVDGFCCLSVKVNTDG 93 Sequence:

283224 segs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	85.5	۳.		7	T13703	tamA protein - fru
7	81		1163	~1	JE0366	tight junction pro
3	77	16.5	775	7	146236	junction
4	^		1116	7	154378	X104 prote
5	76.5		853	7	2973	hypothetical prote
9	7		2054	7	T46612	
7	4		538	7	159291	
80	74.5		2450	7	S71625	protein-tyrosine-p
σ	Э.	15.7	2055	~	T30259	multiple PDZ domai
10	72	15.4	387	7	G97295	periplasmic trypsi
11	72		717	7	T33295	
12	71.5	٠.	494	7	S27696	
13	71.5		503	7	T50791	hypothetical prote
14	71.5	15.3	2294	7	167630	S
15	71.5		2466	7	I67629	protein-tyrosine-p
16	71.5		2490	Н	A54971	protein-tyrosine-p
17	71		2172	~	T20145	hypothetical prote
18	70	15.0	1136	7	AB1581	0
19	7		1281	~	T00346	hypothetical prote
20	ω.	4	394	7	S74643	_
21	68.5	₹.	408	٦	E42409	
22	œ.	4.	408	Н	F41858	biphenyl dioxygena
23	8	4	782	~	T48246	ribonuclease II-li
24	8	4	823	7	AF3361	endopeptidase La (
25	68	14.6	352	7	T22159	hypothetical prote
56	Θ	₹.	723	7	T14765	hypothetical prote
27	67.5	14.5	505	7	The same	alpha-syntrophin -
28	67	4	295	7	E69398	
59	67	14.3	682	7	AG2118	serine/threonine k

4

Gaps

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A;MOlecule type: mRNA A;Residues: 1-1163 <COL> A;Cross-references: GB:AF085184; NID:93820579; PIDN:AAC95469.1; PID:93820580

Query Match 17.3%; Score 81; DB 2; Length 1163; Best Local Similarity 35.3%; Pred. No. 1.6; Matches 24; Conservative 16; Mismatches 20; Indels

flagellar biosynth	nypornericai prote carboxy-terminal p	flagellar biosynth	hypothetical prote	different proteins	dynein heavy chain	probable fructokin	proteinase (EC 3.4	topoisomerase IV,	vacB protein - The	nitrate reductase	aminopeptidase Atu	proteinase DO VC05	threonine ammonia-	B. subtilis SpoVG
AE0745	AC3202 JH0263	B55546	T22166	AH1227	B54802	F71020	AG0433	A87494	H72341	S16292	AE3189	F82307	E75502	AD1462
77	v (7	7	7	7	Н	7	~	7	7	П	7	~	7	7
692	539	692	1034	1136	4367	310	457	695	710	982	384	456	568	102
14.3	14.1	14.1	14.1	14.1	14.1	14.0	14.0	13.9	13.9	13.9	13.8	13.8	13.8	13.6
67	99	99	99	99	99	65.5	65.5	65	65	65	64.5	64.5	64.5	63.5
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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tama protein - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster
C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C.Accession: T13703
R.Takahisa, M.; Togashi, S.; Suzuki, T.; Kobayashi, M.; Murayama, A.; Kondo, K.; Miya Genes Dev. 10, 1783-1795, 1996
A.Title: The Drosophila tamou gene, a component of the activating pathway of extramac A.Reference number: Z17700; MUID:96312452; PMID:8698238
A.Accession: T13703
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tight junction protein, ZO-2 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C;Accession: JE0366
R;Collins, J.R.; Rizzolo, L.J.
Biochem. Biophys. Res. Commun. 252, 617-622, 1998
A;Title: Protein-binding domains of the tight junction protein, ZO-2, are highly cons A;Reference number: JE0366; MUID:99057550; PMID:9837755
A;Accession: JE0366
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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Best Local Similarity 33.8%; Pred. No. 0.63;
Matches 27; Conservative 11; Mismatches 29; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: tamou (tam)
A;Cross-references: FlyBase:FBgn0003177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||| | |:|
460 NGVTREEAVLFLLSLQDRID 479
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RESULT 1
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A;Introns: 41/3; 110/1; 151/2; 194/1; 232/1; 342/3; 390/3; 528/1; 551/2; 628/1; 674/2
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A;Cross-references: EMBL:AJ001320; NID:g2959978; PIDN:CAA04681.1; PID:g2959979
                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-853 <SAN>
A;Cross-references: EMBL: U41035; PIDN: AAB37028.1; GSPDB:GN00028; CESP:TIOA3.1
A;Experimental source: strain Bristol N2; clone T10A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multi PDZ domain protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
C;Accession: T46612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T10A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riullmer, C.; Schmuck, K.; Figge, A.; Lubbert, H.
FEBS Lett. 424, 63-68, 1998
A,Title: Cloning and characterization of MUPP1, a novel PDZ domain protein.
A;Reference number: 223104; MUID:98196865; PMID:9537516
A;Accession: T46612
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVIGG-----NLTGIFIHRV-TPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLE 70
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                                                                                                                                                                                                                                                                     R;Sansone, J.; Nhan, M. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid T10A3. A;Reference number: 220675 A;Accession: T29736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 76.5; DE 34.2%; Pred. No. 3.5; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB ;
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; Pred. No. 11;
13; Mismatches
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ilarity 32.5%;
Conservative 13
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Matches 27; Conservative
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Matches 25; Conserv
                      567 VREDAVL 573
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A;Gene: CESP:T10A3.1
                                                                                                                                                                                                                                              C; Accession: T29736
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62
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MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.5%; Score 77; DB 2; Length 775; Larity 34.3%; Pred. No. 2.8; Conservative 15; Mismatches 23; Indels
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IVREDAVL 542
                                                                                                          63 VL-EDITL 69
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11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74.5;
Pred. No. 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1145 VSHHAAVDILQNAPEDVTL 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.08;
30.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 --YEASEPLFKAVLEDTTL
A; Reference number: S40280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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G97295
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                                         C. Accession: 159291
R;Ahn, A.H.; Yoshida, M.; Anderson, M.S.; Feener, C.A.; Selig, S.; Hagiwara, Y.; Ozawa, Proc. Natl. Acad. Sci. U.S.A. 91, 4446-4450, 1994
R;Ahn, A.H.; Yoshida, M.; Anderson, M.S.; Feener, C.A.; Selig, S.; Hagiwara, Y.; Ozawa, Proc. Natl. Acad. Sci. U.S.A. 91, 4446-4450, 1994
A;Title: Cloning of human basic Al, a distinct 59-Kpa dystrophin-associated protein ence A; Reference number: 159291; MUID: 94240154; PMID: 8183929
A; Accession: 159291
A; Accession: 159291
A; Accession: 159291
A; Accession: 159291
A; Mesidues: 1-538 <-RES>
A; Residues: 1-538 <-RES>
A; Residues: 1-538 <-RES>
A; Cross-references: GB:L31529; NID: 91066339; PIDN: AAA81523.1; PID: 91066340
C; Genetics:
A; Gene: GDB: SNT2B1; 59-DAP
A; Gross-references: GB: 371344; OMIM: 600026
A; Map position: 8923-8924
C; Superfamily: GLGF domain homology
F; 118-191/Domain: GLGF domain homology
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A; Residues: 1-2450 cCHI>
A; Cross-references: EMBL:D83966; NID:g1232103; PIDN:BAA12158.1; PID:g1232104
A; Experimental source: strain DBA/2; cell line MEL 745A
R; Wolf, B.B.; Brown, M.D.
FBBS Lett. 376, 177-180, 1995
A; Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si
A; Reference number: S67987; MUID:96105375; PMID:7498536
A; Accession: S67987
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A; Residues: 1338-1354, Kr, 1356-1447, Kr, 1449-1454 (RE2>
A; Cross-references: (B:134581; NID:9806295, PIDN:AAC42055.1; PID:9806296
A; Cross-references: (B:134581; NID:9806295, PIDN:AAC42055.1; Mieringa, B.
R; Hendriks, W.: Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A; Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
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N;Alternate names: epidermal growth factor-binding protein; serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 21-Jun-2002
C;Accession: S71625; S67987; I81210; I81209; S40290
R;Chida, D.; Kume, T.; Mukouyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, FBBS Left. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very A;Reference number: S71625; MUID:95145716; PMID:7843407
                            Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecules: 1329-1354, K',1356-1447, R',1449-1454 <RES>
A;Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
A;Accession: 181209
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1098-1102 < WOL>
A; Residues: 1098-1102 < WOL>
A; Experimental source: submaxillary glands
R; Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
S; Science 268, 411-415, 1995
A; Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
A; Reference number: 159595; MUID:95232528; PMID:7536343
A; Accession: 181210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 16.0%; Score 74.5; D Best Local Similarity 35.6%; Pred. No. 3.4; Matches 32; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LFKAVLEDTTLEEAVGLLRRVDGFCCLSVK 88
Species: Homo sapiens (man)
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Date: 22-Oct-1999
R;Stapson, E.H.; Sulfolk, R.; Jackson, I.J.
Genomics 59, 102-104, 1999
A;Title: Identification, sequence, and mapping of mouse multiple PDZ domain protein g A;Reference number: 220797; MUID:99326529; PMID:10395806
                                                                                                                                                                                                                                                                                                                      A.Gene: Ptpn13
A.Map position: 5
A.Superfamily: position: 5
A.Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homolog C.Superfamily: phosphorotein; phosphoric monoester hydrolase; transmembrane protein; ty F.566-860/Domain: protein 4.1 membrane-binding domain homology GLGS positions of GLGF domain homology GLG2>
F.1361-1437/Domain: GLGF domain homology GLG2>
F.1495-1574/Domain: GLGF domain homology GLG3>
F.1769-1814/Domain: GLGF domain homology GLG3>
F.1769-1814/Domain: GLGF domain homology GLG4>
F.1760-1814/Domain: GLGF domain homology GLG4>
F.1760-1814/Domain domain homology GLG3>
F.1760-1814/Domain domain homology GLG3
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A;Molecule type: mRNA
A;Residues: 1-2055 <SIN>
A;Cross-references: EMBL:A131869; NID:94150877; PIDN:CAA10523.1; PID:94150878
A;Experimental source: strain C57/BL6 X CBA F1; whole brain
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A;Molecule type: mRNA
A;Residues: 2266-2372 <HEN>
A;Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1863-1937/Domain: GLGF domain homology <GLG5>
F;2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2374/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2380/Binding site: substrate phosphate (Arg) #status predicted
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Length 494;

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R; Mackawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A; Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membr
A; Reference number: I53483; MUID:94116679; PMID:8287977
A; Accession: I67630
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                        A;Cross-references: GB:M80674; NID:g153488; PIDN:AAA67518.1; PID:g153499
A;Notes requence extracted from NCBI backbone (NCBIN:87744, NCBIP:87747)
A;Notes sequence extracted from NCBI backbone (NCBIN:87744, NCBIP:87747)
B;Bibb, M.J.: Biro, S.; Motamedi, H.; Collins, J.F.; Hutchinson, C.R.
EMBO J. 8, 2727-2736, 1989
A;Title: Analysis of the nucleotide sequence of the Streptomyces glaucescens tcml gen A;Reference number: 805972; MUID:90060035; PMID:2684656
A;Accession: S05976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T50791
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T30N20_90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 LADQGMERFSRIADLGGGGDGWFLAQILRRHPHATGLLMDLPRVAASAGPVLEEAKVADRV 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NLTGIF--IHRVTPGS------AADQM 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 TVLPGDFFTDPVPTGYDAY -- LFKGVLHNWSDERAVTVLRRV 419
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 71.5; Di
30.4%; Pred. No. 6.6;
live 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LAFQGDALLEQISVIGG------
                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X15312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: 5
A, Introns: 220/3; 255/3; 312/3
A, Note: T30N20_90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-503 <BEV>
                                 A; Molecule type: DNA
A; Residues: 1-494 <SUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-17 <BIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 VAVKGMC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T50791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: 167630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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C; Species: Streptomyces glaucescens
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Oct-1999
C; Accession: B42276; S05976; S257696
R; Summers, R.G.; Wendt-Plenkowski, E.; Motamedi, H.; Hutchinson, C.R.
J. Bacteriol. 174, 1810-1820, 1992
A; Title: Nucleotide sequence of the tcmII-tcmIV region of the tetracenomycin C biosynthe
dehydratase-O-methyl transferase.
A; Reference number: A42276; MUID:92193265; PMID:1548230
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4888, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A.Reference number: A96900; MUID:21359325; PMID:21359325
A.Accession: G97295
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-387 < KUR>
A.Residues: 1-387 < KUR>
A.Residues: GB:AE001437; PIDN:AAK81154.1; PID:g15026290; GSPDB:GN00168
A.Experimental source: Clostridium acetobutylicum ATCC824
C.Genetics: A.Scene CAC3218
C.Superfamily: Escherichia coli trypsin-like proteinase; GLGF domain homology; trypsin h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F26D11.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33295
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, May 1998
A;Doscription: The sequence of C. elegans cosmid F26D11.
A;Reference number: 221316
A;Reference number: 221316
A;Reference number: 221316
A;Reference number: 2713295
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AF068716; PIDN:AAC17752.1; GSPDB:GN00023; CESP:F26D11.11
A;Reperimental source: strain Bristol N2; clone F26D11
C;Gene: CESP:F26D11.11
A;Map position: 5
A;Introns: 34/2; 119/2; 226/1; 302/3; 368/3; 576/2; 623/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 GKVIKPFVGIVGGDIKVRSQDNMKGVYVKEVVPGSGAAKAGLRPSDIILELNGQ----- 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 GDALLEQISVIGG-----NLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVD----YEASEPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 72; DB 2; Length 387; 23.7%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 -RILSTNDIGSIVSSSKIGDKVPC---KVNRNG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 FKAVLEDTTLEEAVGLLRR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 29.1% nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 23.79
Matches 22; Conservative
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form 3

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Gaps

1,

33;

Length 503; Indels

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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 - C:Species: Homo sapiens (man)
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R:Reference number: 153483; MUID:94116679; PMID:8287977
A; Reference number: 153483; MUID:94116679; PMID:8287977
A; Reference number: 153483; MUID:94116679; PMID:8287977
A; Reterence number: 153483; MUID:941210; PIDN:BAA04751.1; PID:9452192
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology, GLGS2-
C; Reywords: phosphoric monoester hydrolase
F; 574-8687Domain: GLGF domain homology GLGS2-
F; 2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
F; 2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
A;Residues: 1-2294 <RES>
A;Cross-references: GB:D21211; NID:9452193; PIDN:BAA04752.1; PID:9452194
A;Cross-references: GB:D21211; NID:9452193; PIDN:BAA04752.1; PID:9452194
C;Superfamilty: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C;Keywords: phosphoric monoester hydrolase
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1187-1258/Domain: GLGF domain homology <GLG2>
F;2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>
                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                 1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                         DB 2; Length 2294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.3%; Score 71.5; DB 2; Length 2466; 28.6%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                       30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                         Query Match 15.3%; Score 71.5; D
Best Local Similarity 28.6%; Pred. No. 39;
Matches 24; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
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Job time: 10.125 secs
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hes 24; Conservative
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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 22, 2003, 08:49:35; search time 3.625 Seconds (without alignments) 1064.082 Million cell updates/sec on: Run

US-09-767-215-2\_COPY\_568\_660 Perfect score:

1 QVTMLAFQGDALLEQISVIG......GLLRRVDGFCCLSVKVNTDG 93 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

Minimum

length: 0 length: 2000000000 sed DB DB Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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13.2 906 1 CADO_XENLA	13.1 298 1 DHY2_ARCFU	692 1 FLHA_ECOLI P76298	13.1 870 1 DLG2_HUMAN Q15700	60.5 13.0 326 1 PANE_RHILO Q987n5 rhizobium 1	13.0 414 1 SPYA_RAT P09139	13.0 749 1 SPOT_SPICI	13.0 1026 1 PTP1_CAEEL	1428 1 YA84_SCHPO	13.0 5065 1 EPPL_HUMAN	12.8 236 1 YIN1_STRAM	12.8 330 1	ALIGNMENTS	
61.5	61	61	61	60.5	60.5	60.5	60.5	60.5	60.5	09	09		
34	35	36	37	38	39	40	41	42	43	44	45		

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Q9BXL6; Q9BVB5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
MEDLINE-21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bcl10, induces Bcl10
phosphorylation and NF-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                      Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                                 SEQUENCE FROM N.A. MEDDMed=11278692; M.D., Poyet J.-L., Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Brinvasula S.M., Merriam S., Distefano P.S., Alnemri E.S.; "CARD11 and CARD4 are novel caspase recruitment domain (CARD1/membrane-associated quanylate kinase (MAGUK) family members that interact with BC110 and activate NF-kappab."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1004 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interaction.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cervix, and Colon;
           STANDARD;
                                                                                 2) (Carma 2).
CARD14 OR CARMA2.
                                                                                                                                           NCBI_TaxID=9606;
         CARE_HUMAN
CARE_HUMAN
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CONFLICT
                                                                                                                                                                                                                                                                                                                      Query Match
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DOMAIN
DOMAIN
DOMAIN
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    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcll0-interacting MAGUK protein
                                                                                                                                                                                                                            DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
                                                                                                                                                                                                                                                  FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
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                                                                                                                                                                                                                                                                                                                                 1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Bimpl, a MAGUK family member linking protein kinase C activation
Bcll0-mediated NF-kappa B induction.",
J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benito
   and for
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-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK.

-!- SUBUNIT: CARD14 and Bcll0 bind to each other by CARD-CARD interaction (By similarity).

-!- SUBCELDULAR LOCATION: Cytoplasmic (By similarity).

-!- SUBCELDULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                         100.0%; Score 467; DB 1; Length 1004; 100.0%; Pred. No. 1e-42; 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-2131982; PubMed-11387339;
MEDLINE-2131982; PubMed-11387339;
MCAllister-Lucas L.M., Inchara N., Lucas P.C., Ruland J., B.
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.
                                                                                                                                                                                                                                                                      7469B8B56BE06073 CRC64;
                                                                                                                                                                                                COILED COIL (POTENTIAL).
                                                                                                      SMART; SM00072; Gukc; 1.

SMART; SM00072; Gukc; 1.

PROSTTE; PS50209; CARD; 1.

PROSTTE; PS00086; GUANYLATE_KINASE_1; FALSE_NEG-PROSTTE; PS50106; PDZ; 1.
                                                                                                                                                                                                                     GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      999 AA
    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                        628 KAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 660
                                                                                                                                                                                                                                                                                                                                                                             KAVLEDITLEEAVGLLRRVDGFCCLSVKVNTDG 93
              entities requires a license agreement (or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                               AAH01326
                                          EMBL; AF322642; AAG53403.1; -.
EMBL; AY032927; AAK54453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL; BC001326; AAH01326.1; ALT_INIT.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                        1004 AA; 113299
                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                      107
409
658
990
671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2) (Bimp2).
CARD14 OR BIMP2.
                                                                                                                                                                                      15
128
568
858
858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcn.
Li Q., Cu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARE_MOUSE
                                                                                                                                                                             Coiled coil
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99KF0;
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
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-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE-21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
Garmal, a CARD-containing binding partner of Bcl10, induces Bcl10
phosphorylation and NF KappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-21192234; Pubmed-11278692; M.D., Poyet J.-L., MEDIINE-2119234; Pubmed-11278692; M.D., Poyet J.-L., Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.; CARDII and CARDI4 are novel caspase recruitment domain carpilla associated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      743 QAQQQLLA -> HLLEDHRS (IN REF. 2).
113496 MW; D18350DA12430255 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%; Score 381; DB 1; Length 99
79.6%; Pred. No. 2.1e-33;
.ive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, BC004692; AAH04692.1; -.
InterPro; IPR00619; Guanylate_kin.
InterPro; IPR00178; PDZ.
InterPro; PFR00178; PDZ.
Pfan; PF00595; PDZ, 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50865; GUANYLATE_KINASE_1; FALSE_NEG-PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1147 AA
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF363457; AAK60137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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411
655
986
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Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3) (Carma 1).
CARD11 OR CARMA1
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125
572
854
736
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Q9BXL7;
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O62683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ID 203_C,

AC 06268

DT 16-0C

DT 16-0C

DT 15-JU

DE Tight

DE CCClu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                         INTERACTULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells. Not detected in HeLa Si, Molt-4, A549 and G431 cells.
-!- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS I GRAD DOMAIN.
-!- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-!- SUBPOSCE to contain a SH3 domain which is not detected by PROSITE, Pfam or SWART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                         Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK. Stimulates the
phosphorylation of Bcl10.
-!- SUBUNIT: CARD11 and Bcl10 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 103 CARD.
123 442 COLLED COIL (POTENTIAL).
673 748 PDZ.
966 1133 GUANYLATE KINASE.
808 808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 139; DB 1; Length 11 36.5%; Pred. No. 3.7e-07; Live 17; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:16393; CARD11.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR000419; PDZ.
SMART: SM00228; PDZ.
SMART: SM00228; PDZ.
PROSITE: PSS0209; CARD: 1.
PROSITE: PSS00856; GUANYLATE_KINASE_1; FA PROSITE: PSS00856; GUANYLATE_KINASE_2; FA PROSITE: PSS0106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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nes 31; Conservative
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                                                                                                                                                                                                                           interaction.
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O95049;
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                                 ERRATUM
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Matches
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1D 203_H
1D 203_H
1D 203_H
1D 16-0C
1D
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SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Brower A., Gordon L., Dias J., Ramirez M.,

Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,

A stilwagen S., Atix C., Andracise T., Trankheim M.,

A vila J., Liu S., Atix C., Andreise T., Trankheim M.,

A mico Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,

A maco Keller G., Koopayashi A., Olsen A.S., Carrano A.V.;

A nonan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;

Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;

Serine protease gene cluster.",

Sumitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.

SIMILARITY: CONTAINS 1 S13 DOMAINS.

SIMILARITY: CONTAINS 1 S13 DOMAIN.

SIMILARITY: CONTAINS 1 S13 DOMAIN.

SIMILARITY: SELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 80; DB 1; Length 933; 34.4%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 93 PDZ 1.
195 272 PDZ 2.
394 460 PDZ 3.
489 563 SH3.
675 775 GUANYLATE KINASE.
933 AA; 102800 MW; 680298CFD0615B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50002; SH3; 1. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             898 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC005954; AAC72274.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:11829; TJP3.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001452; SH3.
Pfam; PF00559; PD2, 3.
Pfam; PF00525; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00072; GUKC; 1
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P31016; 1BFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 21; Conserv
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551 VREDAVL 557
NCBI_TaxID=9615;
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ZO2_HUMAN
  SO THE THE TENDER OF THE PRESENCE OF THE PRESE
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                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-98198478; PubMed-9531559;
Haskins J., Gu L., Wittchen E.S., Hibbard J., Stevenson B.R.;
Fac. A noved member of the MAGUK protein family found at the tight
junction, interacts with Zo.1 and occludin.";
J. Cell Biol. 141:199-208(1998).
I. SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND ZO-1.
INTERACTS WITH ORALIN CLAUDINS AND ZO-1.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
ISIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                      Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 protein) (Zona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUANYLATE KINASE.
8091D6132DB9F15D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00652; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00028; PDZ; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-2 (Zonula occludens)
occludens 2 protein) (Tight junction protein 2)
TJP2 OR 202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 78; 34.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF023617; AAC39177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tight junction; SH3 domain; DOMAIN 11 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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        Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   898 AA;
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Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P31016; 1BFE.
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Q95168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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N 123

N 121

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                    MEDLINE-96421547; PubMed=8824195; Beatch M., Jesaitis L.A., Gallin W., Goodenough D.A., Stevenson B.R.; Beatch M., Jesaitis L.A., Gallin W., Goodenough D.A., Stevenson B.R.; "The tight junction protein 20-2 contains three PDZ (PSD-95/Discs-Large/Zo-1) domains and an alternatively spliced region."; J. Biol. Chem. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9
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Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45AB836BBDDB1226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
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Interpro; IPR001478; PDZ.
Interpro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00018; SH3; 1. Pfam; PF00595; PDZ; 3. Pfam; PF00625; Guanylate_kin; 1. SMART; SM00072; GuKc; 1. SMART; SM00228; PDZ; 3. SMART; SM00328; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132085 MW;
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34.3%;
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Best Local Similarity 34...
Loca 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
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1174 AA;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VLEDITL 69
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between
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                                                                                                                                                                                                       Duclos F., Rodius F., Wrogemann K., Mandel J.L., Koenig M.;
"The Friedreich ataxia region: characterization of two novel genes and
                                                                                                                                                                                                                                                                                              MEDLINE=20472049; Pubmed=11018256;
Chlenski A., Ketels K.V., Korovaitseva G.I., Talamonti M.S., Oyasu R.,
Scarpelli D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).

-I ALTERNATIVE PRODUCTS: 4 ISOFORMS; Al (SHOWN HERE), Cl, A2 AND C2;
ARE PRODUCED BY ALTERNATIVE SPLICING AND ALTERNATIVE INITIATION.
-I TISSUE SPECIFICITY: THIS PROPERIN IS FOUND IN EPITHELIAL CELL
JUNCTIONS. ISOFORM AL IS ABUNDANT IN THE HEART AND BRAIN WHEREAS
ISOFORM CL IS EXPRESSED AT HIGH LEEVEL IN THE KIDNEY, PANCREAS,
HEART AND PLACENTA. IN BRAIN AND SKELETAL MUSCLE, ONLY ISOFORM AL
IS DETECTABLE. ISOFORM CL IS FOUND IN NORMAL AS WELL AS IN MOST
IN NORMAL TISSUE.

IN NORMAL TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROFEINS.
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 1086
                                                                                                                                                                                                                                                                                                                              "Organization and expression of the human zo-2 gene (tjp-2) in normal and neoplastic tissues.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlenski A., Ketels K.V., Engeriser J.L., Talamonti M.S., Tsao M.-S., Koutnikova H., Oyasu R., Scarpelli D.G.;
"Lo-2 gene alternative promoters in normal and neoplastic human pancreatic duct cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlenski A., Ketels K.V., Tsao M.-S., Talamonti M.S., Anderson M.R., Oyasu R., Scarpelli D.G.;
"Tight junction protein 20-2 is differentially expressed in normal pancreatic ducts compared to human pancreatic adenocarcinoma.";
Int. J. Cancer 82:137-144(1999).
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
202_HUMAN STANDARD; PRT; 1190 AA. 090DV2; 015883; 09UDV1; 09UDV1; 099839; 16-0CT-2001 (Rel. 40, created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) cocludens 2 protein ZO-2 (Zonula occludens 2 protein) (Tight junction protein 2). TJP2 OR ZO2 OR X104.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-104 FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS A1; C1; A2 AND C2)
                                                                                                                                                                                                                                reduction of the critical region to 300 kb.";
Hum. Mol. Genet. 3:909-914(1994).
                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1493:319-324(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Pancreas;
MEDLINE-99426875; Pubmed=10495427;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99287578; Pubmed-10360833;
                                                                                                                                                                                           MEDLINE-95038744; PubMed-7951235;
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                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM A1).
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                                                                                                      Homo sapiens (Human).
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                                                                                                                                           NCBI_TaxID=9606;
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the Swiss Institute of Bioinformatics and the EMBL outstation
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EMBL; AF043195; AAD20387.2; JOINED.
EMBL; AF043196; AAD20387.2; JOINED.
EMBL; AF043197; AAD20387.2; JOINED.
EMBL; AF177518; AAD20387.2; JOINED.
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occludens 2 protein) (Tight junction protein 2). TJP2 OR 202.
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DOMAIN 10
                               Mus musculus (Mouse)
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Matches 23; Conserv
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                                                                                                            SEQUENCE FROM N.A
                                                                           NCBI_TaxID=10090;
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Q9QXY1;
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   qq
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                                                                                                                                                                                                                                                                                                                                                                    right junction; SH3 domain; Repeat; Membrane; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                A1/A2.
TIGHT JUNCTION PROTEIN ZO-2, ISOFORMS
C1/C2.
FOR ISOFORMS C1/C2.
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0920U1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                 TIGHT JUNCTION PROTEIN 20-2,
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MISSING (IN ISOFORM A2/C2).
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P -> S (IN REF. 1).
FFN -> SFT (IN REF. 1).
FFN -> SFT (IN REF. 1).
K -> N (IN REF. 1).
K -> N (IN REF. 1).
C -> N (IN REF. 1).
C -> S (IN REF. 1).
D -> S (IN REF. 1).
ARLQ -> GPGL (IN REF. 1).
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BE2BE6F181467058 CRC64;
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(IN REF. 5).
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GSYG -> RSFC (IN
EYR -> IRS (IN R
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                   AF177527; AAD56219.2; JOINED.
AF177528; AAD56219.2; JOINED.
AF177529; AAD56219.2; JOINED.
AF177532; AAD56219.2; JOINED.
                                                                              AF083892; AAC33121.1; -.
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34.3%;
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                                                                                                               U84581; AAB41794.1; -.
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Best Local Similarity 34.39
Matches 23; Conservative
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ZOZ_MOUSE
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EMBL;
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                                                                                                                                          STRAIN-CSTRL/6 X CBA;

X MEDLINE-99150392; PubMed=10026224;

X MEDLINE-99150392; PubMed=10026224;

TIOH M., Morita K., Tsukita S.;

TIOH M., Morita K., Tsukita S.;

Toccludin mod alpha catenin ";

Toccludin and alpha catenin ";

Toccludin and alpha catenin ";

To subclic chem. 274:598(-1999).

TO SUBULT: INTERACTS WITH OCCLUDIN.

TO SUBULT: INTERACTS WITH OCCLUDIN.

TO SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE. CYTOPLASMIC SIDE.

TO SUBCELLULAR LOCATION: PRIPHERAL MEMBRANE. CYTOPLASMIC SIDE.

TO SIMILARITY: CONTAINS 1 SH3 DOWAIN.

TO SIMILARITY: CONTAINS 1 GUANTATE RINASE-LIKE DOMAIN.

TO SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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Pred. No. 3.2;
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AA; 131614 MW; F15DA3EBC3F9434F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Membrane.
PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1341872; Tjp2.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00018; SH3; 1.
Pfam; PF00625; PDZ; 3.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; Gukc; 1.
SMART; SM00228; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF113005; AAD19964.1; -.
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50106; PDZ; 3
PROSITE; PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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01-FEB-1995 (Rel. 31, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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   δ
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institution. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                         Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN t junction protein 20-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%; Score 73; DB 1; Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.8%; Pred. No. 4;
ive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B787BA1592661FEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
DOMAIN 187 264 PDZ 2.
DOMAIN 368 434 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 AA
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00856; GUANYLATE_KINASE_1; PROSITE; PS50052; GUANYLATE_KINASE_2; PROSITE; PS50002; SH3; FALSE_NEG. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                               InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
InterPro; IPR001478; PD2.
InterPro; IPR001455; SH3.
Ffam; PF00625; Guanylate_kin; 1.
SMART; SM00275; Guanylate_kin; 1.
SMART; SM00228; PD2; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                         MEDLINE-20069797; PubMed-10601346;
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                                                                                                                                                                                                                                                                                                       EMBL; AF157006; AAF24175.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                      MGD; MGI:1351650; Tjp3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368
467
654
905 AA;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                 STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                 P31016;
                                                 TJP3 OR ZO3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                       Summers R.G., Wendt Plenkowski E., Motamedi H., Hutchinson C.R.; "Nucleotide sequence of the tcmII-tcmIV region of the tetracenomycin C biosynthetic gene cluster of Streptomyces glaucescens and evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                 Multifunctional cyclase-dehydratase-3-0-methyl transferase tomN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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EMBL, X15312; CAB38457.1; -.
PIR; B42276; B42276.
PIR; S27656; S27696.
PIR; S05976; S05976.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR000971; SAM_bind.
Pfam; PF00991; Methyltransf2.
Antibiotic biosynthesis; Multifunctional enzyme; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 AA; 55930 MW; 6E153D32782F66B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 that the tcmN gene encodes a multifunctional cyclase-dehydratase-O-methyl transferase."; J. Bacteriol. 174:1810-1820(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 71.5; 30.4%; Pred. No. 3;
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / ETH 22794 / GLA.0;
MEDLINE-92193265; PubMed=1548230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                     Streptomyces glaucescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methyltransferase.
                                                                                                                                      NCBI_TaxID=1907;
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Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
"Cloning and Characterization of PTPLI, a protein tyrosine phosphatase
with similarities to cytoskeletal-associated proteins.";
J. Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-99329089; PubMed-10400701; Mutthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.; "ZRP-1, a zyvin-related protein, interacts with the second PDZ domain of the cytosolic protein tyrosine phosphatase hPTPIE."; J. Biol. Chem. 274:20679-20687(1999).
                                                                                   PTND_HUMAN STANDARD; PRT; 2485 AA. 012923; 015263; 016826; 015265; 015159; 01607-2001 (Rel. 40, Created) 116-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) (Protein tyrosine phosphatase 1E) (PTP-E1) (hPTPE1) (PTP-EAS) (Protein-tyrosine phosphatase 1E) (PTP-E1) (hPTPE1) (PTP-EAS)
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94116679; PubMed-8287977;
Mackawa K., Inagawa N., Nagamatsu M., Harada S.;
"Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GLGF repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-:- SUBUNIT: Interacts with TRIP6 and FAS receptor through its second
                                                                                                                                                                                                                                                                                                                Banville D., Ahmad S., Stocco R., Shen S.-H.;
"A novel protein-tyrosine phosphatase with homology to both the
cytoskeletal proteins of the band 4.1 family and junction-associated
guanylate kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 1361-1456.
MEDILTB=20170882, Pubmed=10704206;
KOZIOV G., Gehring K., Fitel I.;
"Solution structure of the PDZ2 domain from human phosphatase hPTPIE
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor.";
Biochemistry 39:2572-2580(2000).
-!- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT INHIBITS FAS-INDUCED APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and its interactions with C-terminal peptides from the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
              380 TVLPGDFFTDPVPTGYDAY--LFKGVLHNWSDERAVTVLRRV 419
41 ALRPG---TQIVMVDYEASEPLFKAVLEDTTLEEAVGLLRRV 79
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 269:22320-22327(1994).
                                                                                                                                                                                                                                                                                       TISSUE-Breast carcinoma;
MEDLINE-94350988; PubMed-8071359;
                                                                                                                                                                                       phosphatase 1) (FAP-1).
PTPN13 OR PTP1E OR PTPL1 OR PNP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fibroblast;
MEDLINE=95014139; PubMed=7929060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1216-2490 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett. 337:200-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH TRIP6.
                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Leukemia;
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ domain.
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang H.Y
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                                       -!- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00660; BAND_41_1; FALSE_NEG.
PROSITE; PS00661; BAND_41_2; FALSE_NEG.
PROSITE; PS00661; BAND_41_3; 1.
PROSITE; PS50016; PD2, 3.
PROSITE; PS00183; TYR_PHOSPHATASE_1; FALSE_NEG.
PROSITE; PS500183; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).
MISSTNG (IN ISOFORM 3).
LD -> FH (IN REF. 3).
KDHHWSRGTLRHIS -> DLSRSHCHVYLAHL (IN
                                                                                         -i- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 5 PDZ/DHR DOMAINS.
-i- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAND 4.1-LIKE.
PROTEIN-TYROSINE PHOSPHATASE.
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-> A (IN REF. 3).
-> K (IN REF. 4).
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GL -> A (IN REF. 4).
S -> P (IN REF. 4).
KP -> RS (IN REF. 4).
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PDZ 2.
PDZ 3.
PDZ 4.
PDZ 5.
POLY SER.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001478; PDZ.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; TYY_PP.
Pfam; PF00102; Y_phosphatase; 1.
Pfam; PF001373; Band_41; 1.
Pfam; PF00595; PDZ; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil
                                                                                                                                                                                                                                                                                                                                    EMBL; U12128; AAB60339.1; --
EMBL; D21201; BAA04750.1; --
EMBL; D21211; BAA04751.1; --
EMBL; X80289; CAA5653.1; --
EMBL; X79676; CAA56124.1; --
PDB; 3PDZ; 17-MAR-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0935; BAND41.
PRINTS, PRO0700; PRTYPHPHTASE.
SMART; SM00228; PBZ; 5.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000299; Band_4.1.
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                                                                            FETAL BRAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                               4
                                                                                                                                                                                                                                    ::|::: || ::|: |: || 1090 EITLVNLKKDAKYGLGFQIIGGEKMGRLDLGIFISSVAPGGPADLDGCLKPGDRLISVNS 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Diphenyl and polychlorinated biphenyl degradation.
SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: THE
TWO SUBUNITS OF THE HYDROXXIASE COMPONENT (BPHA AND BPHE), A
FERREDOXIN (BPHF) AND A FERREDOXIN REDUCTASE (BPHG).
SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE
FERREDOXIN REDUCTASE COMPONENTS.
KSQEDTICTMFYYPQKI -> RVKKIPFVPCFTILRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase system ferredoxin--NAD(+) reductase component (EC 1.18.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erickson B.D., Mondello F.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PART OF THE ELECTRON TRANSFER COMPONENT OF BIPHENYL
DIOXYGENASE, TRANSFERS ELECTRONS FROM FERREDOXIN (BPHF) TO
                                                                                                                                                                                                               1 QVTMLAFQGDALLE-QISVIGGNL----TGIFIHRVTPGSAAD-QMALRPGTQIVMVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erickson B.D., Mondello F.J.; "Nucleorite sequencing and transcriptional mapping of the genes "Nucleorite sequencing and transcriptional mapping of the genesenceding biphenyl dioxygenese, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudomonas strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
                                                                                                                                            DB 1; Length 2485;
                                                                                                                                                                             30; Indels
                                                                                     10 GLLDQ -> VARS (IN REF. 4).
276903 MW; BD1B31597C66962B CRC64;
                (IN REF. 4).
G -> A (IN REF. 3).
AA -> G (IN REF. 4).
A -> S (IN REF. 4).
GLLDQ -> VARS (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                408 AA.
                                                                                                                                          15.3%; Score 71.5; D
28.6%; Pred. No. 18;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                    1150 VSLEGVSHHAAIEILQNAPEDVTL 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 174:2903-2912(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92234948; PubMed-1569021;
                                                                                                                                                                                                                                                                                    -----YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M86348; AAB63429.1; -.
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                  1857
                                   1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferredoxin + NADH.
                                 1797 179
1856 189
2069 206
2206 221
2485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; F41858; F41858.
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LB400
                                                                                                                                                                                                                                                                                                                                                                                                            BPHG_BURCE
P37337;
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InterPro; IPR001327; FAD\_pyr\_redox.

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                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robertson G.T., Kovach M.E., Allen C., Ficht T.A., Roop R.M. II;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN
PRESENCE OF ATP. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED
IN THE PROTEIN SUBSTRATE (BY SIMILARITY).
-- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,
cassin and denaturated servim albumin, in presence of ATP.
-- SUBUNIT: HOWOTETRAMER (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          11 ALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIV-----MVDYEASEPLFKAVLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                   Length 408;
                         Pfam; PF00070; pyr_redox; 1.
PRINTS; PR00368; FADPNR.
ProDom; PD000139; FAD_pyr_redox; 1.
Aromatic hydrocarbons catabolism; Flavoprotein; FAD; NAD;
                                                                                                                                                                               FAD (ADP PART) (POTENTIAL).
NAD (ADP PART) (POTENTIAL).
8A52BB01688667A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-JUN-2002 (Rel. 41, Last annotation update)
ATP-dependent protease La (EC 3.4.21.53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812 AA
                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                   14.7%; Score 68.5; 31.6%; Pred. No. 5.
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SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
PROSTIE; PS01046; LON; 1.
PROSTIE; PS01046; LON_SER; 1.
Hydrolase; Serine protease; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA_ATPase_centr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR000205; NAD_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA_ATPase.
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                                                                                                                                                                                                                                           42953 MW;
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                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 DTTLEEAVGLLRRVDG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                  35
173
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Pfam; PF02190; LON; 1.
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                                                                                                                                                                                                                                              408 AA;
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S16.001;
                                                                                                                                                      Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=235;
                                                                                                                                                                               NP_BIND
NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches
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LON_BRUAB
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                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of a novel human serine protease that has extensive homology to bacterial heat shock endoprotease HtrA and is regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray C.W., Ward R.V., Karran E.H., Turconi S., Rowles A., Viglienghi D., Southan C., Barton A., Fantom K.G., West A., Savopoulos J.W., Hassan N.J., Clinkenbeard H., Hanning C., Amegadzie B., Davis J.B., Dingwall C., Livi G.P., Creasy C.L., "Characterization of human HtrA2, a novel serine protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faccio L., Fusco C., Viel A., Zervos A.S.;
"Tissue-specific splicing of Omi stress-regulated endoprotease leads
to an inactive protease with a modified PDZ motif.";
Genomics 68:343-347(2000).
                                                                       Gaps
                                                                                             13 LEQISVIGGNLTG-------IFIHRVTPGSAADQMALRPGTQIVMVDYEA-- 55
                                                                                                                    4 IEOKTPVGGSETGGADGLYAVLPLRDIVVFPHMIVPLFVGREKSIRALEEVMGVDKQILL 63
                                                                                                                                                                                                                      HRA2_HUMAN STANDARD; PRT; 458 AA.
043464: Q9PBZ4: Q9POY3: Q9POY4:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease HTRA2, mitochondrial precursor (EC 3.4.21.-) (High temperature requirement protein A2) (HrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI).
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 134-458, INTERACTION WITH BIRC4, AND MUTAGENESIS OF
                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                 Faccio L., Fusco C., Chen A., Martinotti S., Bonventre J.V., Zervos A.S.,
                                                Length 812;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF SER-306.
MEDLINE-20112822; Pubmed-10644717;
                                                                       33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Chen F., Do A., Do T., Meisler M., Roe B.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       -----SEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTDG 93
               Y SIMILARITY.
B9D07E9F0D7DFDBB CRC64;
                                                Score 68.5; DB 1;
ATP (POTENTIAL).
BY SIMITART#V
                                                                       20; Mismatches
                                                             Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the mammalian cellular stress response.";
Eur. J. Biochem. 267:5699-5710(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 275:2581-2588(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-20428457; PubMed-10971580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Kidney;
MEDLINE-20453195; Pubmed-10995577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21468395; PubMed-11583623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                            89859 MW;
                                                14.78;
                                                             22.68;
                                                                         Conservative
                689
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
     367
689
812 AA;
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ischemia.
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     NP_BIND
ACT_SITE
SEQUENCE
                                                 Query Match
                                                                Best Local
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                                                                                                                                          26
                                                                          Matches
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Procease HITAL.'.

Protein Expr. Purif. 19:227-234(2000).

Protein Expr. Purif. 19:227-234(2000).

I Protein Expr. Purif. 19:227-234(2000).

I Protein Expr. Purif. 2016 Expr. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       MEDLINE-20334437; PubMed=10873535; Savopulos J.W., Carter P.S., Turconi S., Pettman G.R., Karran E.H., Gray C.W., Ward R.V., Jenkins O., Creasy C.L.; "Expression, purification, and functional analysis of the human serine protease HtrA2.";
Suzuki Y., Imai Y., Nakayama H., Takahashi K., Takio K., Takahashi R.; "A serine protease, HtrA2, is released from the mitochondria and interacts with XIAP, inducing cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transit peptide, Transmembrane, Apoptosis, Alternative splicing TRANSIT 131 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM.
MISSING (IN ISOFORM 2).
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Hydrolase; Protease; Serine protease; Zymogen; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE HTRA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAP-BINDING MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001940; Protease2C.
InterPro; IRN001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF184911; AAG13126.1; -.
EMBL; AC006544; -; NOT_ANNOTATED_CDS.
EMBL; BC000096; AAH00096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF020760; AAB94569.2; -.
EMBL, AF141305; AAF66596.1; -.
EMBL, AF141306; AAF66597.1; -.
EMBL, AF141307; AAF66598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00834; PROTEASES2C. SMART; SM00228; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:14348; PRSS25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001478; PDZ.
                                                                                          interacts with XIAP, indu
Mol. Cell 8:613-621(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.278;
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1134
1105
1106
3364
1134
1198
2228
306
238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
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ACT_SITE
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
L -> LARELGAVSLQ (IN ISOFORM 3).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
GEVICAVINTKVTAGISFALPSDRIREFLHRGEKKNSSGI
SGSQRRYICWMMLTLEPSILAELQLREPSPPVQHGWLHKK
VILGSPAHRAGIRPGDVILAIGEQWYQNAEDYYEAVRTQSQ
LAVQIRRGRETLILLYVPREVTE -> VSETSFLPRIPAPGQ
CGKGRRPLIGGCLWRFLSSSLLAISQYPTRSPQHILVLFG
CPHPLLFV (IN ISOFORM 4).
A->M. LOSS OF INTERACTION WITH BIRC4;
LOSS OF INHIBITION OF BIRC4 ACTIVITY.
A->M. LOSS OF INTERACTION WITH BIRC4 AND
OF INHIBITION OF BIRC4 ACTIVITY.
S->M. LOSS OF PROTESSE ACTIVITY.
S->M. LOSS OF PROTESSE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: Zinc (Probable).-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Remard C., Cunnacc S., Demange N., Saptier M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Reissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: ||:| || || : |||| |: 390 GVLIHKVILGSPAHRAGLRPGDVILAIGEQMVQNAEDVYEAVRTQSQL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIFIHRVTPGSAADQMALRPGTQIVMVD---YEASEPLFKAVLEDTTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical zinc metalloprotease RSc1411 (EC 3.4.24.-).
RSC1411 OR RSO5281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ.
InterPro; IPR004387; Zn_Mprotease.
InterPro; IPR0004387; Zn_Mprotease.
InterPro; IPR000130; Zn_MTpeptdse.
SMART; SM00228; PDZ; 1.
TIGREAMS; IIGR00054; mem_zinc_metalprot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.2%; Score 66.5; Di
33.3%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50106; PDZ; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GMI1000;
MEDLINE-21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                             48840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL646064; CAD15113.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
         313
403
458
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                                                                                                                                                                                                                                                                                                                                                                                             458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M50.004;
                                                                                                                                                                                                                                              134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia
                               VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                              MUTAGEN
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YE11_RALSO
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'n
Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
                                                                                                                                                    Gaps
                                                                                                                                                    .;
8
                                                                                                                                                                                            218 VIEQVGLKLLGGPVT---IAEVLPGSAGERAGLRRGDQIVRF---AGQPADQA 264
                                                                                                                                                                             12 LLEQIS -- VIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                                        14.1%; Score 66; DB 1; Length 462; 37.7%; Pred. No. 11;
                           (CATALYTIC) (POTENTIAL).
                                                  ZINC (CATALYTIC) (POTENTIAL).
                                                                                                                                                    Indels
                                                                                             3F2818F8B0C1121B CRC64;
                                                                                                                                                   10; Mismatches 15;
                                                                                                                                                                                                                                                Search completed: January 22, 2003, 08:53:35
Job time : 6.625 secs
                                          POTENTIAL
               Complete proteome.
                            ZINC
                                                                                             49613 MW;
                                                                                                                                                    Conservative
                                                                                             462 AA;
                                                                                                                                     Similarity
               Inner membrane;
                                                                                                                                                   20;
                                      ACT_SITE
METAL
TRANSMEM
                                                                                             SEQUENCE
                                                                                                                        Query Match
                                                                                                                                       Local
                                                                                 DOMAIN
                            METAL
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008783 mus musculu 055164 rattus norv 08Vby0 mus musculu 08Vbv5 mus musculu 099188 mus musculu 01411 homo sapien 055925 mus musculu 02174 rhizobium m 09W2174 rhizobium m 09W2174 rhizobium 092174 rhizobium 092174 rhizobium 092174 rhizobium 092174 rhizobium 092174 rhizobium 092174 mus musculu 014425 homo sapien 064235 mus musculu 0143798 homo sapien 092199 mus musculu 0997199 mus musculu 0997199 mus musculu 0907170 homo sapien 099719 mus musculu 0907170 homo sapien 0907170 homo sapien 0907170 homo sapien 0907170 homo sapien 0907180 mus musculu 0907170 homo sapien 0907170 homo sapien 0907170 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                   Q91y70 rattus norv
Q9jh11 mus musculu
Q920g2 rattus norv
Q8sqg9 oryctolagus
 P70625 rattus norv
               022366 caenorhabdi
028006 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 139; DB 4; Length 1171; 36.5%; Pred. No. 2.3e-06; Live 17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 AA; 134966 MW; FA567ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
               022366
028006
008783
055164
08VBYO
08VBYO
08VBYO
014912
015925
015925
015925
015884
064512
092RR4
064512
092RR4
064513
091283
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Q92IG9
Q9VMF3
Q95V18
Q75970
Q91Y70
Q9JHL1
Q92GG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLJ00120 protein (Fragment). FLJ00120.
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ches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
\begin{array}{c} 2.21\\ 2.25\\ 2.44\\ 2.25\\ 2.44\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\ 2.25\\
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043386 hc
081ea3 hc
09uhv4 hc
081eu6 hc
096pc1 hc
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Q9FD11
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Q9TVW0
Q9KK44
Q96KK44
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Q8TEU6
Q96PC1
Q8TEU7
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Gapop 10.0 , Gapext 0.5
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez, C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Y. C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY051965; AAK93389.1;
                                                                                                                                                                                                                                                                         MEDLINE-21025768; PubMed-11225567;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fei K., Yan L., Zhang J., Sarras M.P. Jr.;
Fould and bloological characterization of a zonula occludens-1
honologue in Hydra vulgaris, named H20-1.";
Dev. Genes Evol. 210:611-616(2000).
EMBL, AF230482; AAK28322.1;
INSP: P29476; 10AV.
InterPro: IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                 Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%; Score 104; DB 5; Length 1695; 40.6%; Pred. No. 0.024; ive 9; Mismatches 15; Indels 14
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Last annotation update)
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Last annotation update)
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    PRT; 1695 AA
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PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
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                                               Created)
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                                             (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 19, I
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                                                                                                            Tight junction protein ZO-1.
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Matches 26; Conservative
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InterPro; IPR000906; ZU5
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SEQUENCE FROM N.A.
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735 VLIL 738
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=96312452; PubMed=8698238;
Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A.,
Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A.,
Kondo K., Miyake T., Udda R.;
"The Drosophila tamou gene, a component of the activating pathway of
extramacrochaetae expression, encodes a protein homologous to
mammalian cell.cell junction-associated protein 20-1.";
EMBL, D83477; BAA11923.1; -.
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                                                                                                                                                                                                                                                   Gaps
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18.3%; Score 85.5; DB 5; Length 1367;
Best Local Similarity 33.8%; Pred. No. 1.9;
Matches 27; Conservative 11; Mismatches 29; Indels 13.
                                                                                                                                                                                                Length 974;
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                                                                                                                                     DZ; 3.
107338 MW; 5FA3A7D7D0922C2E CRC64;
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Last annotation update)
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                                                                                                                                                                                                  18.3%; Score 85.5; Di
33.8%; Pred. No. 1.3;
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InterPro, IPR000619; Guánylate_kin.
InterPro; IPR001478; PD2.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PD2, 2.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PD2; 2.
SMARY; SM00072, GuKc; 1.
SMART; SW00228; PD2; 3.
SWART; SW00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 NGVTREEAVLFLLSLQDRID 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 NGVTREEAVLFLLSLODRID 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 EDTTLEEAV----GLLRRVD 80
                                                                                                                                                                                                                                                                                                                                                                                                   65 EDTTLEEAV----GLLRRVD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0003177; pyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYD OR TAMOU OR CG9763.
                                                                                                                                                    974 AA;
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q12923; 3PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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1445 AA; 156723 MW; A5675FB66676A40E CRC64;

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SEQUENCE
g
                                                                                                                                                                                 Db
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                                                                                                                                                                                                                                                                              Db
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RAIN PEDETRIELEY;

RAIN PEDETRIELEY;

RAIN MEDILINE-20196006; PubbMed=10731132;

RAIN MEDILINE-20196006; PubbMed=10731132;

RAIN MEDILINE-20196006; PubbMed=10731132;

RA Amanatides P.G. Scherer S.E., Hilp P.W., Hoskins R.A., Galle R.F.;

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Borkova D. Botcham M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova D.A., Buller H., Caddeu E., Center A., Chandra I.,

RA Borkova D.A., Buller H., Caddeu E., Center A., Chandra I.,

RA Glodek A., Gody E.L., Downes M. Dugan-Rocha S., Punkov B.C., Dunn P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

A Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

A stand B.M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin Z.,

Lasko P., Lei Y., Levitsky A.A., Li J.J., Morpherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra Bazzolo M., Pittman G.S., Pan S., Pollard J., Woshrefi A.,

Spier E., Spradiling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradiling A.C., Stapleton M., Stupski W.P., Smith H.O.,

Ra Shue B.C., Sladen-Klamos I., Simpson M., Stupski M.P., Smith R.,

Syltskas R. M., Woors F.N., Zhong W., Zhong S., Zho X., Smith H.O.,

Ra Shene S., Zhodon-Klamos I., Simpson M., Stupski M. Wang Z.-Y., Wassaman D.A., Weilsenbach J.,

Ra Shene S., Zhodon-Klamos I., Simpson M., Stupski M., Shong R., Shong 
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; NCBL_Tax1D-7227;
                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                 PRT; 1445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; 012923; 3PD2.
FlyBase; Frg00003177; pyd.
Interpro; IPR000619; Guanylate_kin.
Interpro; IPR001478; pp2.
Interpro; IPR001452; SH3.
Interpro; IPR001906; ZU5.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00625; PDz; 2.
Pfam; PF00791; ZU5; 1.
                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003680; AAF54300.1;
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SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
SMART; SM00218; 2U5; 1.
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY
                                                                                                                                                                                    PYD protein.
PYD OR CG9763.
                                                                 Q9VHK4
                 RESULT 5
                                           Q9VHK4
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RAIN MEDILINE-20196006; PubbMed-10731132;

RADAIN PEDKRALEY;

RADAIN MEDILINE-20196006; PubbMed-10731132;

RADAIN MEDILINE-MEDILINE MEDILINE MEDILINE, RELATION C.R. MAILOS G.L.G.

RADAILI J.F., Agbayani A., An H.-J., Andraws-Pfannkoch C., Baldvin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottlier P.,

RADAILI J.F., Agbayani A., An H.-J., Mandraws-Pfannkoch S.,

RADAILI J.F., Aburely S., Dahlke C., Davenpolt L.B., Brottlier P.,

RADAIL MEDILINE, R., Downes M., Dugan-Rocha S., Platkov S.,

RADAIL M., Cawley S., Dahlke C., Davenpolt L.B., Davies P.,

RADAIL M., Cawley S., Dahlke C., Baser K.,

RADAIL M., Cayley S., Dahlke C., Rerrad C., Ferrad C., Fer
                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                          Gaps
                                                                                                                                                    5 LAFQGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVL 64
                                                                            13;
       Length 1445;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
CG5509 protein (LD32687p).
                                                                    29;
       DB 5;
18.3%; Score 85.5; DF
33.8%; Pred. No. 2.1;
tive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1916 AA.
                                                                                                                                                                                                                                                                                                                                                                     460 NGVTREEAVLFLLSLQDRID 479
                                                                                                                                                                                                                                                                                                 65 EDTTLEEAV----GLLRRVD 80
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY
   Query Match
Best Local Simi
Matches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG6509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VKG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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Methanopyrus
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9YHV2
                                                                                                                                      Q8TVMO;
                                                                                                                         Q8TVM0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9YHV2
                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                    16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Chanzez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003632: AAF33102.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jirally T. N., in T. J., Liou C. M.;
Lin T. N., in T. J., Liou C. M.;
"Aeromonas hydrophila strain CKH-29 prtS1 gene complete cds.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AFC93977; AAG03073.1; -.
MEROPS; S01.274; -.
InterPro; IPR001478; PDZ.
InterPro; IPR00149; PDZ.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 2.
PRINTS; PR00334; PFOTEASESZC.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.0%; Pred. No. 0.65;
Matches 27; Conservative 14; Mismatches 30; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                              Query Match
18.2%; Score 85; DB 5; Length 1916;
Best Local Similarity 31.2%; Pred. No. 3.3;
Matches 20; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                         1916 AA; 209863 MW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50106; PD2; 2.
PROSITE; PS50106; PD2; 2.
PROSITE; PS50340; TRYPSIN.DOM; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 453 AA; 47828 WW; BD55CE2B844E5148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 AA.
                                                                                                 EMBL, AV069586; MAL39731.1; ---
HSSP, P31016; 1BB2.
FYBASS. FB9400013363; CG6509.
InterPro: IPR0010419; PDZ.
InterPro: IPR0010419; PDZ.
InterPro: IPR0010452; SH3.
Ffam; PF00595; PDZ; 3.
SMART; SM00724; GMK; 1.
SMART; SM00326; SH3; 1.
PROSTITE; PS50052; GANNYLATE_KINASE_2; 1.
PROSTITE; PS50105; PDZ; 4.
SEQUENCE 1916 AA; 209863 MW; 32B2A61ABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20, HtrA-like serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeromonas hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=644;
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                                                                                                                                                                                                                                                                                                                                                                                           76 LRRV 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FD11
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Q9FD11
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GDALLEQISVIGGNLT------GIFIHRVTPGSAADQMALRPGTQIVMVDYEA 55

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callus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVTMLAFQGDALLEQISVIGGNLTGIFIHRVTPGSA--ADQMAL-RP-GTQIVMVDYEAS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri Av19
and monophyly of archaeal methanogens.";
EMBL; AE010430; AAM02582.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-RETINA;
MEDLINE=99057550, PubMed=9837755;
Collins J.R., Rizzolo L.J.;
Collins J.R., Rizzolo L.J.;
"Protein-binding domains of the tight junction protein, ZO-2, are highly conserved between avian and mammalian species.";
Highly conserved between avian and mammalian species.";
EMICHERITY: CONPAINS I SH3 DOMAIN.
EMBL; AF085184; AAC95469.1; ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 81; DB 17; Length 334; 35.4%; Pred. No. 1.1; tive 10; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA; 35878 MW; 5940DBBD2133D92B CRC64;
                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SELD OR MK1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1163 AA.
                                                                                                                                                                                                                      334 AA.
                                                                                                             322 IRSFGELRAKIATMGADKQVALGLIR--DG 349
                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                       56 ----SEPLFKAVLEDTTLEEAVGLLRRVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 EPLFKAVLEDITLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                        Methanopyrus kandleri
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Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2320;
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Connolly K.S., Gunning K.M., Davis C.A., Kadner K., Subramanian S., Miguel T., Lewis K.D., Fridlyand J., Alcivare D., Benke J.A., Bondoc M., Bowen E., Chiang A., Critz P., Jaklevic M.A., Lindo K., Lindquist K., Miller C., Patel S., Piscia C., Riley B.E., Rojeski H., Sarmiento R., Yu C., Montenegro M., Aerts A., Chung A., Abrajano A., Rimmerly W., Martin C.H.; Ko C., Beall K., Woolley J.P., Stultz J.L., Kimmerly W., Martin C.H.; Sequencing of human chromosome S."; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ricke D.O., Wagner R.P.;
"Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC04237; AACC04379.1;
HSSP; Q12923; 3PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79.5; DB 4; Length 579; Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%; Score
34.6%; Pred. No. 3.1,
'*** 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001595; cNMP_binding.
InterPro; IPR001478; PDZ.
InterPro; IPR00151; RasGEFN.
Pfam; PF001621; CMP_binding; 1.
Pfam; PF001595; PDZ; 1.
Pfam; PF00189; RasGEFN; 1.
SMART; SM0100; cMP; 1.
SMART; SM001209; RasGEFN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50042; CNMP_BINDING_3; 1.
PROSITE; PS50106; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIA001LB (Fragment). KIA001LB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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043386
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ID O8
AC O8
DT 01
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TISSUB-EMBRYO, AND MAINLY HEAD;

TISSUB-EMBRYO, AND MAINLY HEAD;

TISSUB-EMBRYO, AND MAINLY HEAD;

A Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

A Tanase T., Nomura Y., Tojia S., Komai F., Hara R., Takeuchi K.,

A Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Makamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AK027292; BAB55020.1; -.

R InterPro; IPROU0419; Guanylate_kin.

R InterPro; IPROU1452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MLAF-QGDALLEQISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 ISVIGGNLTGIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEAVGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-3002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14386 fis, clone HEMBA1002417, moderately similar to TIGHT
Junction protein 20-1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.3%; Score 81; DB 13; Length 1163; Best Local Similarity 35.3%; Pred. No. 4.9; Matches 24; Conservative 16; Mismatches 20; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
17.1%; Score 80; DB 4; Length 548;
Best Local Similarity 34.4%; Pred. No. 2.6;
Matches 21; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1163 AA; 130668 MW; 3639431A560B1D4E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0052; GUANYLATE_KINASE_2; 1.
PROSITE; PSS0106; PDZ; 3.
PROSITE; PSS0002; SH3; 1.
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PRINTS; PROJEOD; ZONOCCLUDNS3.
PROSTITE; PSSOODS; GUANYLATE_KINASE_2; 1.
PROSTITE; PSSOOD2; PRD2; 1.
PROSTITE; PSSOOD2; SH3; 1.
HSSP, P31016; 1BE9.
InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PD2.
InterPro: IPR001478; PD2.
InterPro: IPR001472; SH3.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF0055; PD2; 3.
Pfam; PF0018; SH3; 1.
PRINTS; PR01597; ZONOCCLUDNS.
PRINTS; PR01599; ZONOCCLUDNS2.
PRINTS; PR01599; ZONOCCLUDNS3.
SMART; SM0072; Gukc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00228; PDZ; 3.
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Pfam; PF00595; PDZ; 1.
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096KB4
AC 096KB
DT 01-DE
DT 01-DE
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                                                                                                                                Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., "NEDO human cDNA sequencing project."; Submitted (FBE-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AKO74318; BABBS649.1: SEQUENCE 1113 AA; 126109 MW; B12B7DFDDEBC502B CRC64;
                                                                                                                                                                                                                                                                                                                                                  Kawasaki H., Chen E.J., Springett G.M., Graybiel A.M., Housman D.E.; "A new family of Rap guanine nucleotide exchange factors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. "EMBL, AF117947; AAF22004.1; -.. HSSP; Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                 15 QISVIGGNLT--GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA 72
                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                     17.0%; Score 79.5; DB 4; Length 1113; 34.6%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PDZ domain-containing guanine nucleotide exchange factor I.
                                                                                                                                                                                                                                                                                                      Indels
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ29738 fis, clone HEP15081, highly similar to PDZ
domain-containing quanine nucleotide exchange factor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137135 MW; 7AEADFE5CD00646B CRC64;
                                                                                                                                                                                                                                                                                                   12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1204 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001478; PDZ.
InterPro; IPR000651; RasGEFN.
InterPro; IPR0011895; RasGRF_CDC25.
InterPro; IPR0011895; RA_domain.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00595; PDZ; 1.
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Pfam; PF00788; RA; 1.
Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEF; 1.
SMART; SM00100; CNMP; 1.
SMART; SM00218; PDZ; 1.
SMART; SM00314; RA; 1.
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309 VEILRN-NTHLALTVKTN 325
                                                                                                                                                                                                                                                                                                                                                                                             73 VGLLRRVDGFCCLSVKVN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                 Local Similarity
es 27; Conserva
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Best Local S
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Matches
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543 QFSLNGGSEKGFGIFVEGVEPGSEAADSGLKRGDQIMEVNGQN------FENITFMKA 594
                                  593 OFSLNGGSEKGFGIFVEGVEPGSKAADSGLKRGDOIMEVNGON-----FENITFMKA 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
Kuiperij H.B., de Rooij J., Rehmann H., van Triest M.,
Wittinghofer A., Bos J.L., Zwartkruis F.J.T.;
"Characterization of the PDZ-GEFs, a family of guanine nucleotide exchange factors specific for Rapl and Rap2.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF478469; AAL79916.1; -.
SEQUENCE 1391 AA; 157495 MW; CCIB82FA932EB618 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
QISVIGGNLT - - GIFIHRVTPGSAADQMALRPGTQIVMVDYEASEPLFKAVLEDTTLEEA
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Rapl quanine nucleotide-exchange factor PDZ-GEF2B.
Homo sapiens (Human).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro: IPR000595; cNMP_binding.

InterPro: IPR0006198; PDZ.

InterPro: IPR000661; RASGEFO.

InterPro: IPR001895; RASGEFO.

InterPro: IPR001895; RASGEFO.

InterPro: IPR001895; RASGEFO.

InterPro: IPR001895; RA_domain.

Pfam; PF00027; CNMP_binding; 1.
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Anote= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Protein Kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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.e- "Casein kinase II phosphorylation site"
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e= "Protein Kinase C phosphorylation site"
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e= "Tyrosine kinase phosphorylation site"
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.e= "Tyrosine kinase phosphorylation site"
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.e= "Casein kinase II phosphorylation
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e= "Leucine zipper pattern"
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/note= "N-myristoylation site"
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e- "N-myristoylation site"
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/note="cAMP- and cGMP-dependent protein kinase phosphorylation site" 785.793
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/note= "Casein kinase II phosphorylation site"
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759..761
/note= "Protein kinase C phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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1002..1004
/note= "Protein kinase C phosphorylation site"
                 .637
e= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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"Casein kinase II phosphorylation site"
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868..870
/note= "Protein kinase C phosphorylation
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.e= "Casein kinase II phosphorylation
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863
e= "Casein kinase II phosphorylation
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e= "Peroxisomal targetting signal"
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.872 cell attachment sequence"
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800..805
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826..1004
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                                                                            The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders barkinson's disease, inflammatory disorders, haematological infactions, strokes, immune disorders (e.g., candromes), myocardial infactions.
regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell signalling disorder; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antibacterial.
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Pred. No. 7.9e-43;
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                                                Claim 1; Fig 1A-1E; 109pp; English.
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                                                                                                                                                                                                                                                                                                       1004 AA;
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                                                                                       The present sequence is predicted human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bol-10 and stimmlates phosphorylation of Bol-10 or activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders and parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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/note= "Casein kinase II phosphorylation site"
168..171
/note= "Casein kinase II phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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te= "Protein kinase C phosphorylation
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.e= "Casein kinase II phosphorylation
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                                                              Disclosure; Fig 2A-2C; 109pp; English.
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                                                                                                                                                                                                                                                                                                       1139 AA;
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/note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
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592..695
/note= "Casein kinase II phosphorylation site"
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725..728
725..788 "Casein kinase II phosphorylation site"
761..766
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764..767
/note= "Casein kinase II phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
787..789
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te= "Protein kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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:e= "Casein kinase II phosphorylation site"
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te= "Protein Kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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"Tyrosine kinase phosphorylation site"
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e= "Glycosaminoglycan attachment site"
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:e- "Protein kinase C phosphorylation
                                     "Tyrosine kinase phosphorylation
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766..834
/note= "SH3 domain"
776..779
/note= "N-glycosylation site"
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te= "N-glycosylation site"
                                                         "N-glycosylation site"
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282.285
-+o= "Amidation site"
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638..641
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710.715
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698..703
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471..474
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634
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182..18
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The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell CDAR library. Also described are converted to a human and the carborate and CARD-9 and CARD-10 (AMU01205, AMU01206).

The sequences for CARD-9, CARD-10 and CARD-11 interact and rat CARD-9 (AMU01204). CARD-10 and CARD-11 interact with Bol-10 which is thought to activate nuclear factor (NF) kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-10, or CARD-11.

They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD CARD can be used in screening and detection assays (e.g. chromosomal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                             926.929
/note= "casein kinase II phosphorylation site"
/note= "Protein kinase C phosphorylation site"
1003.1006
/note= "assein kinase II phosphorylation site"
1010.1018
                                                                                                                                   note= "Protein Kinase".
872..875
/note= "Casein Kinase II phosphorylation site"
882..1147
/note= "Guanylate Kinase (GUK) domain"
897..900
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Casein kinase II phosphorylation site"
                                                                                                         /note= "N-myristoyiu......859
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                              /note= "Protein kinase C phosphorylation site"
                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                         /note= "Tyrosine kinase phosphorylation site"
1050..1055
                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 14A-14C; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0507533.
2000US-0513904.
2000US-0685791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000; 2000WO-US32716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0168780
                                                                                                                                                                                                                                      .922
              816..819
                                                                                                                                                                                                                                                      /note=
                              /note=
                                                       /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS05389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200140468-A2
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25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2000;
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                The
mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating inflammation. cancer, NF kappab signalling, stress related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiant;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide, useful for treating skin carcinoma or acantholytic diseases such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus -
                                                                                                                                                                                     1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; plakoglobin; cytostatic; osteopathic; dermatological; cardian plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; Maxos disease; extramammary Paget's disease; heart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey-Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                           5
                                                                                                                                Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                               Human plakoglobin interacting protein PLA_2H12, SH3 domain.
                                                                                                                                                           Indels
                                                                                                                                ; Score 146; DB 22;
; Pred. No. 1.9e-10;
12; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Figure 4; 98pp; English.
                                                                                                                                                                                                                                                                                                                                  AAU73249 standard; Protein; 82 AA
                                                                                                                                  37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001WO-EP04872.
                                                                                                                                             46.5%;
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                               Query Match
Best Local Similarity 46.5 Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Roy F, Bonne S,
                                                                                                                                                                                                                                                                 IPSYSRAQQLL 835
                                                                                                                                                                                                                                       IPNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-062246/08
                                                                                                      1147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200185933-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                           AAU73249;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                             Gaps
                                                                                                                                                                                  2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                              peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease, Huntington's disease, hademostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemctactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders
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Zhang J;
                                                                                                                                           5,
AAU73254 represent novel human plakoglobin interacting protein
                   amino acid sequences and related sequences of the invention
                                                                                                     Length 82;
                                                                                                                                           Indels
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Yang Y,
                                                                                                                                             29;
                                                                                                  Score 116; DB 23;
Pred. No. 7.8e-08;
1; Mismatches 29;
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 2079; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAM38934 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 2079.
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Wehrman T, Xu
Goodrich R,
                                                                                                                                         11;
                                                                                                     30.1%;
40.0%;
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191
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2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                         Conservative
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N-PSDB; AAI58090.
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                      PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                           ||| |||| |
|PNYQRAQQLL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                              Query Match
Best Local Simi
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000;
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14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia
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                                                              Sequence
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                                                                                                                                                                                                                                                                                                             09
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been scolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed
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Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                    \text{C.N.S} disorders. Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                       Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
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K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                       Score 116; DB 22;
Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM93822 standard; Protein; 746 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T, Isogai T,
su A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                           30.1%;
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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Les 28; Conserv
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                                                                                                                                                                                                                                                                                                                               350 AA;
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                                                                                                                                                                                                                                                                   specification.
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                                                                                                                                                                                                                                                                                                                                     Seguence
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AAM93822
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Gaps
                                                                                    2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                        Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Leucine zipper homology region"
242..245
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331..334
/note= "Casein kinase II phosphorylation site"
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/note= "Casein kinase II phosphorylation site"
113..118
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/note= "Protein kinase C phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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230..251
                                          Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Protein kinase C phosphorylation
                                                               Indels
                                                                                                                                                                                                                                                                      Human caspase recruitment domain, CARD-10 polypeptide.
                                          30.1%; Score 116; DB 22; 40.0%; Pred. No. 1.2e-06;
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/note= "N-myristoylation site"
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412..415
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                                                               11; Mismatches
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293..296
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                                                                Conservative
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                                             Mac.
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28;
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                      Sequence
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                                           Query Match
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.e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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e= "Casein kinase II phosphorylation site"
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:e= "Casein kinase II phosphorylation site"
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754-756
70ote= "Protein kinase C phosphorylation site"
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ce= "Protein Kinase C phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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.e- "Casein kinase II phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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e- "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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e= "Protein Kinase C phosphorylation site"
"Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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te= "Glycosaminoglycan attachment site"
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te= "Casein kinase II phosphorylation
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.e= "Guanylate kinase (GUK) domain"
                  "Leucine zipper homology
                                                                                                                                                                                                                                                                                                  .661
.e= "N-myristoylation site"
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.e= "N-myristoylation site"
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915..918
/note= "Amidation site"
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te= "N-glycosylation site"
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re= "MAGUK domain"
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'note= "SH3 domain"
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The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated from a human skin CDAR library. Also described are novel human sequences from a human skin CDARD-11 (AAU01205, AAU01207) and rat CARD-9 (AAU01204).

CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease), and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), conductive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for requiating inflammation, cancer, NF kappaB corrected response and apoptosis in human disease. A host call containing a polynucleotide encoding CARD can be used to create transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening
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                                                                                /note= "N-myristoylation site"
1022..1024
/note= "Protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site"
/note= "Casein kinase II phosphorylation site"
                "Protein kinase C phosphorylation site"
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40.0%; Pred. No. 1.8e-06;
ative 11; Mismatches 29;
                                                  /note= "N-myristoylation site" 1021..1026
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2000US-0507533.
2000US-0513904.
2000US-0685791.
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                 /note= "P
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Matches 28; Conservative
947..949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of an addicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasia/Skin fragility syndrome. Au/73245-AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                    Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Naxos disease; extramammary Paget's disease; hard disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of
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                                                                                                                                                                                                                                                                                                                                  (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                               Human plakoglobin interacting protein #3.
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                        AAU73247 standard; Protein; 1032 AA.
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                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-EP04872.
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression profile) or expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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                                                          Mouse ischaemic condition related protein sequence SEQ ID NO:699
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                                                                                                                 Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human endometrial cancer related protein, TJP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102.5; DB Pred. No. 0.00023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 1740-1748; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU84308 standard; Protein; 1736 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000JP-0145977.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-034733/04.
N-PSDB; ABI99666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 26; Conserv
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574 IPNKNRAEQ 582
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                                                                                                                                                                                                                                                                            WO200188188-A2.
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                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa K,
07-MAR-2002
                                                                                                                                                                                                                                                                                                                                          22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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WO200171042-A2.
                                     27-SEP-2001
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                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU73251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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  Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                        The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleic acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules comprises at least 2 nucleic acid molecules captured from 50 fully defined sequences as given in the specification. The nucleic acids are used as an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen protein microarray comprising at least 2 antibodies or its antigen properties from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are specification, fixed to a solid substrate. The methods and arrays are treatment regimes and identification of lead compounds useful for the treatment of endometrial cancer. The present sequence is one of 50 proteins differentially expressed between cancerous and non-cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ?
                                                                                                                                                                                                                                                  Diagnosing endometrial cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant endometrium \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 GDSFYIRTHFEYEKESPYGLSFNKGEVFRAVDTLYNGKLGSWLAIRIGKNHKE--VERGI 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 98.5; DB 23; Length
Pred. No. 0.0008;
9; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 20649.
Human; endometrial cancer; differential expression;
                                                                                                                                                                                                                                                                                                     Claim 33; Page 225-231; 233pp; English.
                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB64619 standard; Protein; 1445 AA.
           DNA microarray, protein microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%;
36.2%;
                                                                                                            31-JUL-2001; 2001WO-US24104.
                                                                                                                                      31-JUL-2000; 2000US-221735P.
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Matches 25, Conservative
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                                                                                                                                                                                                                WPI; 2002-179967/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| :||:|
562 IPNKNRAEQ 570
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                                                                                                                                                                                                                             N-PSDB; ABK35528.
                                                           WO200209573-A2
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                                     Homo sapiens.
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                                                                                   07-FEB-2002
                                                                                                                                                                                       Mutter GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence acta for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Naxos disease; extramammary Paget's disease; hart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey 'Hailey's disease; Darier's disease; ectodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 20649; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%; Score 97.5; DB 22 ilarity 31.9%; Pred. No. 0.00086; Conservative 13; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse tight junction domain ZO-1, SH3 domain.
                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU73251 standard; Protein; 89 AA.
                                                                                                                                                                                                                                                         Li PWD,
23-MAR-2001; 2001WO-US09231.
                                                                  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 22; Conserv
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                                                                                                                                                                           (PEKE ) PE CORP NY
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556 IPNKSRAEE 564
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                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL08722
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(HELI-) HELIX RES INST.
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB93753;
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                     Query Match
                            Ota T,
                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                    AAB93753
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                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                     The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin related diseases include basal cal carcinoma, squamous cell carcinoma, extramammary Paget's disease, Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey's disease or Darier's disease, and ectodermal dysplasialyskin fragility syndrome. AAU73245 - AAU73254 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide, useful for treating skin carcinoma or acantholytic disease such as Grover's and Darier's disease, comprises a protein interacting with human plakoglobin and involved in transduction of plakoglobin related signal to nucleus.
                                                                                                                                                                                                                                                                                                                                                                     2 DSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGTI 60
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                                                                                                                                                                                                                                                                                                                              DB 23; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human stomach cancer expressed polypeptide SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                   31;
                                       (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                             Score 96.5; DB 23
Pred. No. 3.7e-05;
9; Mismatches 31
                                                             Vanlandschoot A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM93968 standard; Protein; 548 AA
                                                                                                                                                      Example 4; Figure 4; 98pp; English
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9905-0159590

200007-0118776

200005-0183322

200007-0183767

200007-0241899
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36.8%;
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02-MAY-2001; 2001WO-EP04872
                    09-MAY-2000; 2000EP-0201668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stomach cancer;
                                                             Bonne S,
                                                                                WPI; 2002-062246/08
                                                                                                                                                                                                                                                                                                          89 AA;
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PNKNRAEQ 66
                                                                                                                                                                                                                                                                                                                                                                                                              PNYSRAQQ 68
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17-FEB-2000;
02-MAY-2000;
09-JUN-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                            Sequence
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                                                             Van Roy
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     Saito K, Yamamoto J;
Otsuki T, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                 New Stomach cancer-associated genes, useful as markers in blood tests for screening for the early stages of the disease \mbox{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GDSFYIRTHFELEPSPPSGLGFTRGDVFHVLDTLHPGPGQSHARGGHWLAVRMGRDLREQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito K,
, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.5; DB 22;
Pred. No. 0.00035;
7; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi K, S
A, Nagai K,
     Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:13422
                                  Wakamatsu A,
                                                                                                                                                                                                                                                               Claim 1; Page 67-69; 242pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB93753 standard; Protein; 548 AA.
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Sugiyama T, Wakamatsu
sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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38.4%;
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27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                  Ishii S, Sugiyama T, W
Kodama T, Midorikawa Y;
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                                                                                                           WPI; 2001-570287/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 AA;
        Isogai T,
                                                                                                                                        N-PSDB; AAI93843
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us-09-767-215-2\_copy\_676\_745.rag

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The present invention describes primer sets for synthesising 5602 [ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 1'-end sequence of an oligonucleotide comprises at least 15 nucleotides where the oligonucleotide which comprises at a 3'-end sequence of the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and the full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the chetction and/or diagnosis of the abnormality of the full-length cDNAs are primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH13628 and AAH13633 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; kinase; enzyme; PKIN-13 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; eplilepsy; Charcot-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96.5; DB 22;
Pred. No. 0.00035;
                                                     Claim 8; SEQ ID 13422; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
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...te= "PDZ domain"
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38.4%;
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Best Local Similarity 38.4
Matches 28; Conservative
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388..46
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391..47
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                   full-length cDNAs
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The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, neurological disorders (e.g. epilepsy, Charoct-Marie-Tooth disease or seizures), call proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as
                                                                                                                                                                                                                                                                                                                                Gandhi AR;
Tribouley CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 GDSFYIRTHFELEPSPPSGLGFTRGDVFHVLDTLHPGPGQSHARGGHWLAVRMGRDLREQ 543
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                                                                                                                                                                                                                                                                                                                                                  , Ding L, Patterson C, Yue H, Baughn MR, Tribouley Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT; Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG; Warren BA, Kearney L, Policky JL, Thangavelu K;
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Pred. No. 0.00068;
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           /note=""PDZ domain"
733..754
/note= "Leucine zipper domain"
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Job time : 15.6425 secs
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38.4%;
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2000US-236499P.
2000US-238389P.
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2000US-232654P.
                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC
                                                                                                                                         31-AUG-2001; 2001WO-US27219
                                                                                                                                                                          2000US-229873P
                                                                                                                                                                                                                                                                      2000US-240542P
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429..439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukemia or lymphoma)
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                                                                            WO200218557-A2.
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29-SEP-2000;
06-OCT-2000;
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Ramkumar J,
                                                                                                          07-MAR-2002
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Sequence 21, Application US/09562737
Fatent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 724
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Best Local Similarity
US-09-562-737-28
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TYPE: PRT
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Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 27, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 27, Appli
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Sequence 21, Appl
Sequence 27, Appl
Sequence 8, Appli
Sequence 9, Appli
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429.229 Million cell updates/sec
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                                                                                                                   January 22, 2003, 08:52:30 ; Search time 4.79839 Seconds
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1 GDSFYIRVNLAMEGRAKGEL......MKDTAAHGTIPNYSRAQQQL 70
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              GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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US-09-023-731-1
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US-08-448-170-8
US-08-100-709-4
US-08-176-865-4
US-08-779-046-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                    Run on:
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Sequence 11,
Sequence 15,
Sequence 23,
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                  Sequence 2
Sequence 1
Sequence 1
                                                                                                                      Sequence
Sequence
Sequence
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US-09-562-737-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 11;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
US-08-404-445-3

US-09-562-731-22

US-09-374-450A-170

US-09-374-451-9

US-09-171-461-48

US-09-171-461-48

US-08-483-101-15

US-08-349-867-23

US-08-349-867-23

US-08-239-476-27

US-08-239-476-27

US-08-598-305A-23

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-598-305A-35

US-08-639-923A-23

US-08-639-923A-23
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; Pred. No. 6.3;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%;
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AMENAL INFORMATION DAVIGE A.
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 615589el Bacillus thuringiensis Isolate Denoted
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1074 GRGYILRVTAYKEGYGEGCVTIH--EIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1227;
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                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 58; DB 29.9%; Pred. No. 59; Live 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 102D.C1
TELECOMMUNICATION INFORMATION:
TELEPRAN: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION: 424
                                                                                                                                                                                          APPLICATION NUMBER: US/08/448,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1227 amino acids
                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                  CURRENT APPLICATION DATA:
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TITLE OF INVENTION: B.t.
TITLE OF INVENTION: B.c.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-08-448-170-8
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 20; Conserv
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Florida
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                                       32606
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                                                                                                        COMPUTER:
                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    4 FYIRVNLAME-----GRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: Synthetic Sequence
                                                              CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
US-09-562-737-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.2%; Score 58.5; DB 4; Length 724; Best Local Similarity 31.4%; Pred. No. 27; Matches 22; Conservative 7; Mismatches 32; Indels
                                                                                                                                                Score 62.5; DB 4; Length 724;
Pred. No. 8.4;
9; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE OF INVENTION: LDL Receptor Signaling Pathways
TITLE REFERENCE: UTSWOOF, 2000-05-01
CURRENT APPLICATION NUMBER: US/09/562,737
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2:
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09562737 Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08448170
Patent No. 5723758
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cummings, David A. APPLICANT: Cannon, Raymond J.C. APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                      ORGANISM: Artificial Sequence
                                                                                                                                                    Query Match
Best Local Similarity 31.0%;
Matches 22; Conservative
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-562-737-27
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US-09-562-737-27
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                                              FEATURE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-UUL-1993
ATTONEY/AGENT INFORMATION:
NAME: BGOLf, Chilstopher
REGISTRATION NUMBER: 27633
  APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5616319
GENERAL INFORMATION:
                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                     27633
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Best Local Similarity 29.9%;
Matches 20; Conservative 15
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                                                                ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 276
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                 amino acid
                          FILING DATE: 19 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-176-865-4
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel STREET: 1601 Market Street, 36th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1074 GRGXILKVTAYKEGYGEGCVTIH--EIENNTDELKFKNCEEEEVYPTDTGTCNDYTAHQG 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; Score 58; DB 4; Length 122
29.9%; Pred. No. 59;
tive 12; Mismatches 31; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
CLASSIFICATION WORDER: US 08/448,170
FILING DATE: 3-ANY-1995
CLASSIFICATION NUMBER: M/S 102DCD1
FELEPHONE: (352) 375-5800
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 amino acids
                                                       FILING DATE: 31-0CT-1997
CLASSIFICATION: 800
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08100709
Patent No. 5322687
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.9% Matches 20; Conservative
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ZIP: 19103
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US-08-100-709-4
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APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
APPLICANT: GONZALEZ Jr., Jose M.
ATITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIVET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                 4; Gaps
                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
Length 1229;
                                                  31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
; Score 58; DB 1;
; Pred. No. 59;
12; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                  GENERAL INFORMATION:
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                 1134 TAACNSR 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                  19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-881-340-4
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                                                                           RESULT 9
US-08-779-046-4
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tan, Yuping
APPLICANT: Jany, Christine S.
APPLICANT: GONZALEZ Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
CORRESPONDENCE ADDRESS:
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                                                                                            4; Gaps
                                                                                                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
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59;
                                                       DB 1; Length 1229;
                                                                                            31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania STATE: 2IP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                       Score 58; DB
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRELL APPLICATION NUMBER: US/08/474,038
PELING DATE: 07-JUN-1995
CLASSIFICATION STATE
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,865
FILING DATE: 30-DEC-1993
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLF, Christopher
RECISTRATION NUMBER: 27633
RECISTRATION NUMBER: 27633
RECISTRATION NUMBER: 27633
FELECHONE: 215-757-1590
INFORMATION FOR SEQ 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08474038 Patent No. 5679343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Donovan, William P.
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29.9%;
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29.9%;
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LENGTH: 1229 amino acids
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Best Local Similarity 29.99
Matches 20; Conservative
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-474-038-4
protein
                                                       Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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, MOLECULE TYPE:
US-08-176-865-4
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APPLICANT: Donovan, William P. APPLICANT: Tan, Yuping APPLICANT: Tan, Yuping APPLICANT: Tan, Yuping APPLICANT: Jany, Christine S. APPLICANT: Gonzalez Jr., Jose M. TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5 NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS AND SECUENCES: 5 CORRESPONDENCE ADDRESS:
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APPLICANT: Tan, Yuping
APPLICANT: Tan, Yuping
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYET5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1229;
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                                                                                                                                                                                                                                                                    ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
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; Pred. No. 59;
12; Mismatches 3:
                                                                                                                                                                                                                                                                                                ADDRESSEE: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/779,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NOMBER: 05/00/19,040
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EGOLf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECHONE: 215-757-1590
INFORMATION: CR. SEQ. ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08881340 Patent No. 5942658 GENERAL INFORMATION:
Sequence 4, Application US/08779046 Patent No. 5854053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.9%;
Matches 20; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1229 amino acids
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09023731
Patent No. 6291648
GENERAL INFORMATION:
APPLICANT: Kawamura, Yukio; Morita,
APPLICANT: Kawamura, Yukio; Morita,
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
TITLE OF INVENTION: GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%; Score 57.5; Di 32.6%; Pred. No. 1.8;
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 2975/1997
FILING DATE: 13-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: KENNETH H. SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 3479-4000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFONE: (212) 758-480
TELEFAN: (212) 758-480
TELEFAN: (212) 758-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORFEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MTCROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,731
FILING DATE: 13-FEB-199
PRIOR APPLICATION DATA: PSEB-1997
APPLICATION NUMBER: 19-29275/1997
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 3479-4000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 158-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 1758-4800
TELECOMMUNICATION 2580 ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.99
Best Local Similarity 32.69
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-023-731-4
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                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-09-023-731-1
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                                                                                                                                                                                                                                                                                                                                          LENGTH:
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    TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTM-FQGCGCWHAHRVNSYTMKDTAAH-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.0%; Score 58; DB 2; Length 1229; 29.9%; Pred. No. 59; tive 12; Mismatches 31; Indels
                                                                       ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel
                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGBNT INFORMATION:
NAME: EGOLf, Christopher:
REGISTRATION NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09023731
Sequence 4, Application US/09023731
Sequence 4, Application US/09023731
Setuent No. 6291648
GENERAL INFORMATION:
APPLICANT: Kawamura, Yukio; Morita,
APPLICANT: Akihir: Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
TITLE OF INVENTION: GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                          STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/023,731
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.9%
Matches 20; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-881-340-4
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
TITLE OF INVENTION: TO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 FYIRV----NLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHG 58
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE:
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-562-737-24
                                      ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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 DB 4; Length 566;
                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Indels
                                                                                                                                                                                                                                       GENERAL INPORTATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION:
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 724
                                                                                               16 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 58
                                                                          15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%; Score 57.5; DB 4; 28.2%; Pred. No. 36; Live 14; Mismatches 28;
                                     9; Mismatches
14.9%; Score 57.5; 1
32.6%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82, Application US/08469260A Patent No. 6451578
                                                                                                                                                                                                      Sequence 24, Application US/09562737 Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.29
Matches 20; Conservative
                                      14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 FIPSKRRSERR 497
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 Query Match
Best Local Similarity
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ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-469-260A-82
                                                                                                                                                                     RESULT 13
US-09-562-737-24
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                     Matches
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APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No.
TITLE OF INVENTION: Lepidopteran-active Toxins
NUMBER OF SEQUENCES: 4
ADDRESSEE: DAVID R. SALIWANCHIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 YVQHIWHVPDRTMFPELXCNHLXRMPCYRSNHRVGHWKGPNRSSIQK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 HCNEVLHVTD-TMFQGCGCWHAHRVNSYTMKDTAAHGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56.5; DB 4;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: DAVID R. SALIWANCHIK
2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERNEC/FOCKET WUNBER: MA39.C1.D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-040-751-3; Sequence 3, Application US/08040751; Patent No. 5407825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                               TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.6%;
31.9%;
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LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                 1422 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800
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linear
                                                                                                                                                                                                                                                                                                                                                                                          single
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAINESVILLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                               LENGTH: 1422 amir
TYPE: amino acid
STRANDEDNESS: sir
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CLASSIFICATION:
                                                                                CLASSIFICATION:
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                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-469-260A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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Sequence 2, Appli
Sequence 5, Appli
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Sequence 4, Appli
                                                                                (without alignments) 500.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     January 22, 2003, 08:49:35; Search time 2.82258 Seconds
                                                                                                                 US-09-767-215-2_COPY_676_745
386
1 GDSFYIRVNLAMEGRAKGEL......MKDTAAHGTIPNYSRAQQQL 70
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                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-78-5548-4

0 US-09-911-969-4

0 US-09-911-969-1

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US-09-919-497-59
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US-09-767-215-5
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                                                                                                                                                                                                   122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Sequence 11, Appl
Sequence 2, Appli
Sequence 15, Appl
Sequence 21, Appl
Sequence 33, Appl
Sequence 475, App
Sequence 178, Appl
Sequence 1183, Appl
Sequence 1183, Appl
Sequence 1183, Appl
Sequence 128, Appli
Sequence 136, Appli
Sequence 128, Appli
Sequence 136, Appli
Sequence 128, Appli
Sequence 128, Appli
Sequence 128, Appli
Sequence 136, Appli
Sequence 136, Appli
Sequence 136, Appli
Sequence 137, Appli
          Sequence 104, App
Sequence 270, App
Sequence 253, App
Sequence 215, App
Sequence 21139, App
Sequence 21, Appl
Sequence 48, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1004;
                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09767215

Patent No. US20020081636A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-142001

CURRENT FILING DATE: 2001-01-22

PRIOR FILING DATE: 2001-01-22

PRIOR FILING DATE: 2000-02-09

NUMBER OF SEQ ID NOS: 10

SOUTHARD: FALSEQ for Windows Version 4.0

SEQ ID NO.

LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09767215
Patent No. US20020081636A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
      US-09-808-602-104

US-09-808-602-104

US-08-424-550B-170

US-10-108-605-233

US-09-764-864-1139

US-09-813-453A-21

US-09-813-453A-21

US-09-826-660-21

US-09-826-660-21

US-09-826-660-21

US-09-826-660-23

US-09-826-660-23

US-09-826-660-23

US-09-826-660-23

US-09-826-660-23

US-09-824-761-35904

US-09-844-761-35904
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US-10-016-447-7
US-09-764-864-1428
US-09-912-020-355
US-09-912-020-355
US-09-923-302-612
US-09-874-198-7
US-09-874-288-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 386; DB 10;
Pred. No. 3.5e-41;
Mismatches 0;
                                                                                                                                                                                   US-10-001-857-178
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100.0%; Pr
tive 0;
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99
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11155
11156
11163
11186
11551
75
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNYSRAQQQL 70
US-09-767-215-2
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US-09-767-215-5
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                     61
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Sequence 82, Appl Sequence 59, Appl Sequence 14, Appl Sequence 15, Appl Sequence 1641, Appl Sequence 1641, Appl Sequence 696, Appl

US-09-742-684-4 US-09-764-877-1641 US-09-925-302-696 US-10-076-840-6

US-09-976-059-14 US-09-976-059-15

US-09-965-313-4 US-09-732-234-6 US-09-784-859-6

Sequence 4, Appli Sequence 1, Appli Sequence 38, Appl

Sequence 6, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli

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PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 156
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US-09-785-548-4
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                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 98, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
CURRENT FILLNG DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
                                                                                                                                                                            Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.6%; Score 145; DB 9; Length 1247; 46.5%; Pred. No. 2.5e-10;
                                                                                                                                                                                                      Indels
                                                                                                                                                                         100.0%; Score 386; DB 10;
100.0%; Pred. No. 4.1e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
           CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                         Query Match
Best Local Similarity 100.0°
Matches 70; Conservative
FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 46.5
Matches 33; Conservative
                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-767-215-5
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957 IPSYSRAQQLL 967
                                                                                                                                                                                                                                                                                                  60 IPNYSRAQQQL 70
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US-10-032-159A-8
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                                                                                                         LENGTH: 1138
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APPLICANT: AVENTIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF
FILE REFERENCE: STOOMS
CURRENT APPLICATION NUMBER: US/09/785,548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                               Length 1736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kawamura, Yukio; Morita,
Akihiro; Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
GENE ENCODING SAME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 NSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGPSCW 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW 41
                                                                                                                                                                 Score 98.5; DB 10
Pred. No. 0.00032;
9; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09911969 Patent No. US20020137896Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/09785548
; Patent No. US20020155577A1
NUMBER OF SEQ ID NOS: 100
SOFWRARE: Patentin version 3.0
SEQ ID NO 98
LENCTH: 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%;
ilarity 32.5%;
Conservative
                                                                                                                                                                    Query Match 25.5%;
Best Local Similarity 36.2%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-98
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Best Local Similarity
Matches 13; Conserv
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562 IPNKNRAEQ 570
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Gaps

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TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/09866562

Patent No. US20020009758A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Switzer, Anne
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 FYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQ---GCGCWHAHRVNSYTMKDTAAH
                                                                                                                                      DB 10; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.8%; Score 57; DB 10; Length 1050; Best Local Similarity 28.1%; Pred. No. 35; Matches 16; Conservative 10; Mismatches 17; Indels 1
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                         15 RAKGELQVHCNEVLHVTDTMFQGCG---CWHAHRV--NSYTMK
                                                                                                                    14.9%; Scor. 32.6%; Pred. No. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: ABBOTT LABORATORIES D377/AP6D
T: 100 ABBOTT PARK ROAD
ABBOTT PARK
                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESTI
APPLICANT: THOWAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
           TYPE: amino acid
                                                                                                                                                                                Matches 14; Conservative
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CORRESPONDENCE ADDRESS:
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US-09-866-562-38
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                                                                                                                                                            Best Local Similarity
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US-09-866-562-38
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US-09-911-969-1
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                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kawamura, Yukio; Morita,
Akihiro; Izumo, Koji.; Saka, Tomohide.
TITLE OF INVENTION: ANTITUMOR PROTEIN AND
GENE ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 RSQGDLTSSQHEIVHFTDVFIAGSGPISCTYARHIIDNTSTTK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
PRIOR DATE: 24-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,731
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: JP 29275/1997
FILING DATE: 13-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: KENNETH H. SONNENPELD
REGISTRATION NUMBER: 34.79-4000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,969
FILING DATE: 24-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,731
FILING DATE: 13-FEB-1998
APPLICATION NUMBER: JP 29275/1997
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H. SONNENFELD
RECISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 3479-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.9%; Score 57.5; DB
Best Local Similarity 32.6%; Pred. No. 0.94;
Matches 14; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-911-969-4
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TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
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Patent No. US20020137896A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 57
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
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US-09-911-969-1
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US-09-976-059-15
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US-09-742-684-4
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| Sequence 59, Application US/09919497
| Sequence 59, Application US/09919497
| Patent No. US20020106662a1
| GENERAL INFORMATION:
| APPLICANT: Mutter, George L. |
| TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225 |
| CURRENT APPLICATION NUMBER: US/09/919, 497 |
| PRIOR APPLICATION NUMBER: US 60/221,735 |
| PRIOR APPLICATION NUMBER: US 60/221,735 |
| NUMBER OF SEQ ID NOS: 100 |
| SOFTWARE: PatentIn version 3.0 |
| SEQ ID NO 59 |
| LENGTH: 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels
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             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56.5;
Pred. No. 57;
                                                                                                                                                                                5527.PC.01
                                                                                                     CLASSIFICATION: 435435
ATTORNEY/AGENT INCRMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2625
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09976059
Patent No. US20020164747A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
IBM PC compatible
                                                                                                                                                                                                                                  TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%;
ilarity 31.9%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.1%; ll Similarity 29.6%; 21; Conservative
                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-424-550B-82
                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-919-497-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 530 FIPSKRRVERR 540
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Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIPNYSRAQQQ 69
                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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US-09-976-059-14
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Vale, Wylie W.
Tsuchida, Kunihiro
TITLE OF INVENTION: CLOUNG AND RECOMBINANT PRODUCTION OF
RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                      3789 GAEVYRMYTSGSTGRPKGVVTTHQNLVDLATDT-----CWGPTPRVLFHAPHAFDASSY 3842
                                                                                                                                                                                                                                                                                                                                                     Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW------HAHRVNSY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2011-10-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 4999
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 17;
                                                                                                                                                                                                                                                                                                     Length 4999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...νκελοκΕΕ: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Sulte 2000
STATE: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                   Score 54.5; DB 9;
Pred. No. 4.6e+02;
3; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.5; DB 9;
Pred. No. 6.2e+02;
2; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MADDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09976059; Patent No. US20020164747A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09742684 Patent No. US20010039036A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Actinoplanes sp. US-09-976-059-15
                                                                                                                                                                                                                                 ; ORGANISM: Actinoplanes sp. US-09-976-059-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Farnet, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
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Query Match 13.5%
Best Local Similarity 26.0%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                               51 -- MKDTAAHGTIPNYSR 65
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Best Local Similarity ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: SITE
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US-09-925-302-696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 409
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1641, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT APPLICATION HOWBER: US/09/764,877
FILO Application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,123
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08 08/300,584
FILING DATE: 02-SEP-1994
APPLICATION NUMBER: US 07/7880,220
FILING DATE: 08-MAY-1991
APPLICATION NUMBER: US 07/773,229
APTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.5; D
Pred. No. 55;
4; Mismatches
                                                                                                                                                                                                                                                                                                              NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9927
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
APPLICATION NUMBER: US/09/742,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECLLE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-742-684-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 KGNL-VSWNELCHITETMARGLAYLH 300
                     FILING DATE: 19-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 KGELQVHCNEVLHVTDTMFQGCGCWH 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-546-9392 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.6 Best Local Similarity 46.2 Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-764-877-1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1641
LENGTH: 121
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (20) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                    ; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (111) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  18 FFXRLSLAVLPRMMKCSGMISAHCNXRLPGSSNSLAS----AHRVAGITGACHHAQLIF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YIRVNLAMEGRAKGELQVHCN------EVLH--VTDTMFQGCG-----CWHAHR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 YIRPNIAQK-RMQGSLEAHVNGFRFTSVRGDKVDILYNNIKHALFQPCDGEMIIVLHFHL 86
                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 696, Application US/09925302

Patent No. US2002004941A1

GRNERAL INFORMATION:

APPLICANT: Rosen et al.

FILE PREFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR PEPLING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR PELING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 896

SOTWWARE: Patentin Ver. 2.0

SEQ ID NO 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%; Score 52; DB 10; Length 409; ilarity 27.0%; Pred. No. 49; Conservative 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                     13.5%; Score 52; DB 10; Length 121; 26.0%; Pred. No. 12; tive 8; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                          4 FYIRVNLAMEGR -- - AKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYT --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 22, 2003, 08:52:54
Job time : 3.82258 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

January 22, 2003, 08:49:35 ; Search time 5.3629 Seconds (without alignments) 1254.807 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_676\_745 386 1 GDSFYIRVNLAMEGRAKGEL.....MKDTAAHGTIPNYSRAQQQL 70 score: Perfect

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	hypothetical prote	tight junction-ass	tight junction pro	04 prote	tight junction pro	unction	tamA protein - fru	hypothetical prote	Q,	3-hydroxy-3-methyl	transforming prote	transcription requ	probable retroelem	bacterio-opsin act	hypothetical prote		glutamine-fructose	DNA polymerase III	microtubule-associ	hypothetical prote	hypothetical prote	D14R protein - var	hypothetical prote	$\subseteq$	hypothetical prote	probable transposa	probable sulfate a	early E2A DNA-bind	centrosome-associa
SUMMARIES	ID	· ·	A46431	3	154378	JE0366	A47747	T13703	T00346	HYRTTH	D70185	C36365	AI3184	H84495	F84176	B83505	T23215	AI2238	G82100	A55665	E82386	T26727	A72175	T32811	JW0092	T15771	T36152	G81256	ADA	T13802
	DB	7	~	7	7	7	~	7	7	-	7	~	7	~	~	~	~	~	7	~	N	~	7	7	7	7	7	~	Н	7
	Length	1034	1745	775	1116	1163	1736	1367	1281	687	431	206	299	411	864	227	415	541	1164	989	105	161	372	779	1050	865	349	386	517	1096
æ	Query	7.	ė.	9	25.9	S.	ď.	25.3	0.	ف	δ.	15.4	S	S	15.4			15.2					•	٠	•	٠	14.5	•	14.5	14.5
	Score	10	102.5	101	100	100	98.5	97.5	78.5	63.5	09	59.5	59.5	59.5	59.5	29	59	58.5	58.5	58	57	57	57	57	S		26		26	26
	Result No.	 	7	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

C;Accession: A46431 C;Accession: A46431 R;Itoh, M.; Nagafuchi, A.; Yonemura, S.; Kitani-Yasuda, T.; Tsukita, S.; Tsukita, S. J. Cell Biol. 121, 491-502, 1993 A;Title: The 220-kD protein colocalizing with cadherins in non-epithelial cells is id

A; Reference number: A46431; MUID:93252986; PMID:8486731

A; Accession: A46431 A; Status: preliminary

C; Species: Mus musculus (house mouse) C; Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

tight junction-associated protein ZO-1 - mouse

A; Molecule fype: nucleic acid A; Residues: 1-1745 <1TO> A; Cross-references: GB:1014340; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371 A; Experimental source: F9 cells A; Note: sequence extracted from NCBI backbone (NCBIN:131200, NCBIP:131201) C; Superfamily: guanylate kinase homology; GLGF domain homology

C28A5.1 protein (c	hyoscyamine (6S)-d	membrane glycoprot	SAR DNA-binding pr	hypothetical prote	hypothetical prote	Vif protein - Maed	spore coat protein	polyprotein - deng	5-methyltetrahydro	nonstructural prot	genome polyprotein	genome polyprotein	polyprotein - deng	titin - rabbit (fr	hypothetical prote
S43579	A40005	HLBECM	T06379	T10665	T35547	JQ1163	F69604	PQ0507	D83404	A25817	GNWVDP	GNWVJA	JS0219	S20901	T23867
~	٦	-	7	7	7	7	7	~	~	7	-	-	7	7	7
1223	344	368	550	855	1678	231	513	614	166	885	3388	3391	3391	6805	238
14.5	14.4	14.4	14.4	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.1
26	55.5	55.5	55.5	55.5	55.5	52	52	52	52	52	55	52	52	55	54.5

## ALIGNMENTS

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A)Reference number: 21955
A)Reference number: 219525
A)Reference number: 219525
A)Reference number: 219526
A)Recession: 122166
A)Status: preliminary: translated from GB/EMBL/DDBJ
A)Rolecule type: DNA
A)Rolecule type: DNA
A)Residues: 1-1034 <MIL>
A)Residues: EMBL: 268298; PIDN: CAA92607.1; GSPDB: GN00022; CESP: F44D12.1
A)Reportinental source: clone F44D12
C)Genetics:
A)Rep position: 4
A)R
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hypothetical protein F44D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 105.5; DB 2;
35.2%; Pred. No. 9.1e-05;
Live 12; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3%,
Best Local Similarity 35.2%,
Matches 25; Conservative
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|IPSSTTVYQAI 821
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                                                                                                                                                                                              C; Accession: T22166
R; Coles, L.
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A46431
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C; Accession: A47747
R;Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J. Proc. Natl. Acad. Sci. U.S.A. 90, 7834-7838, 1993
A;Title: The tight junction protein 20-1 is homologous to the Drosophila discs-large A; Reference number: A47747; MUID:93361541; PMID:8395056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are highly cons
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A;Molecule type: mRCL
A;Residues: 1-1163 <COL>
A;Residues: 1-1163 <COL>
A;Cross-references: GB:AF085184; NID:93820579; PIDN:AAC95469.1; PID:93820580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                             tight junction protein, 20-2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
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                                                                                             GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
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A;Residues: 1-1736 <WIL>
A;Cross-references: GB:L14837; NID:g292937; PIDN:AAA02891.1; PID:g292938
C;Superfamily: quanylate kinase homology; GLGF domain homology
C;Keywords: alternative splicing; membrane protein; phosphoprotein
F;15-94/Domain: GLGF domain homology <GLG1>
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: JE0366
R; Collins, J.R.; Rizzolo, L.J.
Biochem. Biophys. Res. Commun. 252, 617-622, 1998
A; Title: Protein-binding domains of the tight junction protein, 20-2, A; Reference number: JE0366; MUID:99057550; PMID:9837755
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llarity 36.2%; Pred. No. 0.0012;
Conservative 9; Mismatches 32;
No. 0.00048;
smatches 29;
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37.7%; Pred. No. 0.0005;
tive 9; Mismatches 28
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   39.1%; Pred. No. 0.00 tive 7; Mismatches
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Matches 26; Conservative
      Local Similarity 39.1%
nes 27; Conservative
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659 IPNKSRAEQ 667
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          Best Loca
Matches
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C;Species: Canis lupus familiaris (dog)
C;Accession: Ide26
C;Accession: Ide236
C;Accession: Ide266
C;Acces
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                         Gaps
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C; Genetics:
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9
                                                                                                                                      Length 1745;
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C;Superfamily: guanylate kinase homology; GLGF domain homology
F;37-116/Domain: GLGF domain homology <GLG1>
F;731-879/Domain: guanylate kinase homology <GKI>
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Best Local Similarity 39.1%; Pred. No. 0.00024;
Matches 27; Conservative 7; Mismatches 29; Indels
                                                                                                                                                                                                         Indels
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Hum. Mol. Genet. 3, 909-914, 1994
A; Title: The Friedrich ataxia region: characterization of
A; Reference number: 154378; MUID:95038744; PMID:7951235
                                                                                                                                      Score 102.5; DB 2;
Pred. No. 0.00038;
9; Mismatches 31;
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1116 <RES>
             F;27-106/Domain: GLGF domain homology <GLG1>
F;428-498/Domain: GLGF domain homology <GLG3>
F;645-794/Domain: guanylate kinase homology <GKI>
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                                                                                                                                      Query Match 26.6%;
Best Local Similarity 37.7%;
Matches 26; Conservative
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including the amino end of the mature protein, were \boldsymbol{c} in testes, brain, and pituitary predominantly in a so
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A) Note: sequence extracted from NCBI backbone (NCBIN:142522, NCBIN:142524, NCBIP:1425
A) Note: this report is a correction to A36165
R; McKie, N.; Dando, P.M.; Brown, M.A.; Barrett, A.J.
Biochem J. 309, 203-207, 1995
A; Title: Rat thimet oligopeptidase: large scale expression in Escherichia coli and ch A; Reference number: S55999; MUID:95344370; PMID:7619057
                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Note: this is an engineered sequence expressed in Escherichia coli
R;Pierotti, A.; Dong, K.W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 29, 10323-10329, 1990
A;Fitle: Wolecular cloning and primary structure of rat testes metalloendopeptidase
A;Reference number: A36165, WUID:91084500; PMID:2261476
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C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C; Accession: D70185
R; Fraser, C. M.; Casjens, S.; Huang, W. M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, A; Authors: Smith, H.O.; Venter, J.C.
A; Huthors: Smith, H.O.; Venter, J.C.
A; Reference number: A70100; MUID:98065943; PMID:9403685
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1992 #sequence_revision 17-Nov-1995 #text_change 07-May-1999
C; Accession: 388760, A54152; S55999; A36165
R; McKie, N.; Dando, P.M.; Rawlings, N.D.; Barrett, A.J.
Biochem. J. 295, 57-60, 1993
A; Title: Thimmet oligopeptidase: similarity to 'soluble angiotensin II-binding A; Reference number: S38760; MUID:94029935; PMID:8216239
A; Accession: S38760
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                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-687 <MCK>
A; Residues: 1-087 <MCK>
R; Pierotti, A:; Dong, K.W.; Glucksman, M.J.; Orlowski, M.; Roberts, J.L.
Biochemistry 33, 622, 1994
A; Reference number: A54152; MUID:94114549; PMID:8286394
A; Contents: corrections
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Best Local Similarity 30.0%; Pred. No. 9.5;
Matches 18; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 320-350;578-597,'F',599-687 <PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: significant sequence differences A; Molecule type: mRNA A; Cross-references: GB:M61142 A; Note: parts of this sequence, including t C; Comment: This enzyme is found in testes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-9 <MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S55999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A54152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo saplens (man) (insquency)
C; Decies: Homo saplens (man)
C; Species: Homo saplens (man)
C; Decies: J. 1319, 1998
A; Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A; Reference number: Z14086; MUID:98290545; PMID:9628881
A; Accession: T00346
A; Status: preliminary translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1281 (ANG)
A; Residues: 1-1281 (ANG)
A; Residues: EMBL:AB011155; NID:93043689; PIDN:BAA25509.1; PID:93043690
A; Experimental source: brain; clone HJ0729
C; Genetics:
A; Note: KIAA0583
C; Superfamily: guanylate kinase homology
C; Superfamily: guanylate kinase homology
C; L102-1270/Domain: guanylate kinase homology
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N'Alternate names: endo-oligopeptidase A; endopeptidase 24.15; Pz-peptidase; soluble med
                                                                                                                                                                                                                                                                      C; Accession: T13703
R; Takahisa, M.; Togashi, S.; Suzuki, T.; Kobayashi, M.; Murayama, A.; Kondo, K.; Miyake, Genes Dev. 10, 1783-1795, 1996
A; Title: The Drosophila tamou gene, a component of the activating pathway of extramacroc A; Reference number: Z17700; MUID:96312452; PMID:8698238
A; Accession: T13703
A; Accession: T13703
A; Accession: T13703
A; Molecule type: mRNA
A; Residues: 1-1367 < TAK>
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                                                                                                                                                                                                   Species: Drosophila melanogaster
Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
Accession: T13703
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Llarity 34.9%; Pred. No. 0.25;
Conservative 10; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                          tamA protein - fruit fly (Drosophila melanogaster)
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; Pred. No. 0.00
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.3%;
Best Local Similarity 31.9%;
Matches 22; Conservative 1
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nes 22; Conserv
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       562 IPNKNRAEQ
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1013 IPS 1015
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Description activator-like protein [imported] - Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001
F84176
R; Ng. W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky j. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja. Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                       probable retroelement pol polyprotein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Date: OD-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C.Aaccession: H84495 (S.D. Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Mature 402, 761-768, 1999 (A.T.) (A. Shen, M.) A; File: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA A;Residues: 1-864 <STO> A;Residues: GB:AE004437; NID:910579808; PIDN:AAG18778.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002093; NID:94263646; PIDN:AAD15368.1; GSPDB:GN00139 C;Genetics:
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-411 <STO>
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A; Map position: 2
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R.Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
R.Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. 10, 6654-6654.1990
A.Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhib
A.Reference number: A36365; MUID:91061774; PMID:1701021
A.Reference number: A36365; MUID:91061774; PMID:1701021
A.Ression: C36365
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-206 <AGNSS
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-206 <AGNSS
A.Cross-references: GB:M55177
C. Superfamily: ras transforming protein; translation elongation factor Tu homology
C. Keywords: GTP binding; nucleotide binding; P-loop
F.11-24/Region: uncleotide-binding motif A (P-loop)
F.12-126/Region: GTP-binding motif
F.13-126/Region: GTP-binding stak/L motif
F.13-126/Region: GTP-binding state: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: ll-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: A1184
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
Farp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                        transforming protein homolog MRAS3 - Rhizomucor racemosus
C;Species: Rhizomucor racemosus
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C;Accession: C36365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.4%; Score 59.5; DB 2; Length 206; Best Local Similarity 37.0%; Pred. No. 8.2; Matches 17; Conservative 6; Mismatches 12; Indejs 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 299;
                                                            Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSFY-----IRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 MEGRAK----GELQVHCNEVLHVTDTM---FQGCGCWHAHRVNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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C;Superfamily: conserved hypothetical protein HI1364
                                                               15.5%; Score 60; DB 2;
llarity 38.5%; Pred. No. 16;
Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.4%; Score 59.5; Di
Best Local Similarity 25.3%; Pred. No. 12;
Matches 24; Conservative 10; Mismatches
                                                                                                                                                                                                                  || | || || :::| |::||: | :
LAFNGIQKGHMRLHVNKILHLLKTKY 391
                                                                                                                                                                              10 LAMEGRAKGELQVHCNEVLHVTDTMF 35
         A; Experimental source: strain B31
                                                                                       Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AI3184
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-299 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: Atu5206
                                                               Query Match
                                                                                                                                                                                                                                       366
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Gaps

6

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B83505
hypothetical protein PA1118 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83505
R;Stcver, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathch, Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83505
A;Status: pre-liminary
A;Molecule type: DNA
A;Residues: 1-227 <STO>
A;Cross-references: GB:AE004542; GB:AE004091; NID:99947034; PIDN:AAG04507.1; GSPDB:GN001
C;Gentetics:
A;Gene: PA1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 FYIRVNLAMEGRAKGELQVH--CNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.3%; Score 59; DB 2; Length 227; Best Local Similarity 28.8%; Pred. No. 10; Matches 17; Conservative 7; Mismatches 33; Indels
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Qý Dp Search completed: January 22, 2003, 08:54:42 Job time : 8.3629 secs

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5.1.3
Compugen Ltd.
  version :
                                           - protein search, using sw model
GenCore
Copyright (c) 1993
                                         OM protein
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Run on:

January 22, 2003, 08:49:35; Search time 2.72849 Seconds (without alignments) 1064.082 Million cell updates/sec

US-09-767-215-2\_COPY\_676\_745 386

1 GDSFYIRVNLAMEGRAKGEL..........MKDTAAHGTIPNYSRAQQQL 70 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		mus m	_	рошо	P58660 mus musculu	Q9qxy1 mus musculu		Q95168 canis famil	Q9udy2 homo sapien	_					O9y1c1 lytechinus		051628 borrelia bu		-			bacillus			060566 homo sapien	_	Q03745 bacillus th	P24397 hyoscyamus	_	m	Q9h4d5 homo sapien	7703	P27914 dengue viru
SUMMARIES	. QI	CARE_HUMAN	CARE_MOUSE	CARB_HUMAN	CARA_HUMAN	CARA_MOUSE	ZO3_MOUSE	ZO1_MOUSE	ZOZ_CANFA	ZO2_HUMAN	ZO2_MOUSE	ZO1_HUMAN	ZO3_HUMAN	ZO3_CANFA	MEPD_RAT	EMAP_LYTVA	DLG4_MOUSE	HMDH_BORBU	RAS3_RHIRA	BCAT_CAEEL	DP3A_VIBCH	EMAP_STRPU	C1BE_BACTU	C1BB_BACTU	C1BD_BACTZ	BU1B_HUMAN	DNB2_ADE07	C1EB_BACTA	HY6H_HYONI	VGH3_HCMVA	COTA_BACSU	NXF3_HUMAN	METE_PSEAE	POLG_DEN2T
	DB		П	Н	Н	Н	~	Н	Н	Н	-	П	Н	_	-	Н	-	П	H	Н	Н	П	1	Н	-	-	П		Н	-	-	_	٦,	П
	Query Match Length	1004	666	1147	1032	1021	905	1745	1174	1190	1167	1736	933	868	989	664	724	431	202	415	1159	989	1227	1229	1231	1050	517	1174	344	368	513	531	766	1683
dP	Query	100.0	73.4	37.8	30.1	27.5	27.2	26.6	26.2	25.9	25.6	25.5	25.0	24.5	16.5	16.2	16.2	15.5	15.4	15.3	15.2	15.0	15.0	15.0	15.0	14.8	14.5	14.5	14.4	14.4	14.2		٠	14.2
	Score	386	283.5	146	116	106	105	102.5	101	100	66	98.2	96.5	94.5	63.5	62.5	62.5		59.5		58.5	28	28	28	28	57	26	Ŋ	55.5	ď.	52	52	22	22
	Result No.	-	7	e	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P12823 d genome po P07564 d genome po P14340 d genome po P09980 escherichia Q91651 salmonella P78352 homo sapien P29990 d genome po P29991 d genome po P27770 tomato yell P45813 mycobacteri O58498 pyrococus	Q08890 mus musculu
POLG_DENZP POLG_DENZD POLG_DENZN REP_SOLI REP_SALTY ROLG_LUMAN POLG_DENZ6 POLG_DENZ6 POLG_DENZ7 RS13_MYCBO Y762_PYRHO	IDS_MOUSE
	Н
3388 3391 3391 673 674 767 3391 3391 115 1123	563
113.90	13.9
888 8888 8888 8888 8888 8888 8888 8888 8888	53.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - I- SUBCELLULAR LOCATION: Cytoplasmic.
- I- SUBCELLULAR LOCATION: Expressed in placenta. Also detected in HeLa SISUE SPECIFICITY: Expressed in placenta. Also detected in HeLa SI cells, but not in the other cancer cell lines tested.
- I- SIMILARITY: CONTAINS I CARD DOMAIN.
- I- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
- I- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                  CARE_HUMAN STANDARD; PRT; 1004 AA.
Q9BXL6; Q9BVB5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0
phosphorylation and NF-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK. Stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE—21192234; PubMed=11278692;
MEDLINE—21192234; PubMed=11278692;
Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.;
"CARDII and CARD14 are novel caspase recruitment domain
(CARD)/membrane—associated guanylate kinase (MAGUK) family members
Lhat interact with BCIIO and activate NF-kappaB.";
J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation of Bc110.
-!- SUBUNIT: CARD14 and Bc110 bind to each other by CARD-CARD interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
SEQUENCE OF 1-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cervix, and Colon;
                                                                                                                                                                                  CARD14 OR CARMA2.
                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                 2) (Carma 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRATUM.
                   CARE_HUMAN
RESULT 1
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SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

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 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                           GUANYLATE KINASE.
DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                                GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
FTSPRRCRSTLGWASALSWADVKRSAHL (IN REF. 2;
                                                                                                                                                                                                                                                                                                                                                             676 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bimpl, a MAGUK family member linking protein kinase C activation to Bcll0-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                   1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benito
                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EWBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcl10 and IKK.
-!- SUBUNIT: CARD14 and Bcl10 bind to each other by CARD-CARD interaction (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                      Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21381892; PubMed-11387339;
MCALLISTET-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
Li Q., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                 7469BBB56BE06073 CRC64;
                                                                                                                                                                                          CARD. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                      Score 386; DB 1;
Pred. No. 4.2e-40;
0; Mismatches 0;
                                                                                                                                        GUANYLATE_KINASE_1; FALSE_NEG.
GUANYLATE_KINASE_2; 1.
PDZ; 1.
                                                                                                                                                                                                                                                                        AAH01326
                                                      EMBL, AY032927; AAK54453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL, BC001326; AAH01326.1; ALT_INIT.
INTERPRO, IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                            EMBL; AF322642; AAG53403.1; -.
                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 82-743 FROM N.A.
                                                                                                                                                                                                                                                                                  1004 AA; 113299
                                                                                                                                                                                                                                                                                           Query Match
Query Match
Best Local Similarity 100.vv
Best Local Similarity 100.vv
                                                                                                                                   PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLAT
PROSITE; PS50052; GUANYLAT
PROSITE; PS50106; PDZ; 1.
                                                                                                              SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                           107
409
658
990
671
                                                                                                                                                                                                                                                                                                                                                                                                            136 PNYSRAQQQL 745
                                                                                                                                                                                                                                                                                                                                                                                                61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;

 (Bimp2).
 CARD14 OR BIMP2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                  Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Q., Che
Nunez G.;
                                                                                                                                                                                                               DOMAIN
DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
-!- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected by PROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-21255663: PubMed=11356195; Gaide O., Home M., Tschopp J.; Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; Gaide O., Martinon F., Micheau O., Bonnet D., Induces Bcl10 phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21192234; PubMed=11278692; Berlin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L., Sherlin J., Wang L., Guo Y., Jacobson M.D., Alnemri E.S.; Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.; "CARDII and CARDI4 are novel caspase recruitment domain CARDI4 are soscoiated quanylate kinase (MAGUK) family members that interact with Bcll0 and activate NF-kappaB."; J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 QAQQQLLA -> HLLEDHRS (IN REF. 2)
113496 MW; D18350DA12430255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 283.5; DB ]
Pred. No. 2.3e-27;
4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS0209; CARD; 1.
PROSITE: PS0209; CARD; 1.
PROSITE: PS00866; GUANULATE_KINASE_1;
PROSITE: PS50052; GUANULATE_KINASE_2;
PROSITE: PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                   EMBL; AF363457; AAK60137.1; -. EMBL; BC004692; AAH04692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.48;
75.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
411
655
986
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 PNYSQAQQQL 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3) (Carma 1).
CARD11 OR CARMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BXL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                               Interaction.

-1- SUBCELLUIAR LOCATION: Cytoplasmic.
-1- SUBCELLUIAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, thymus, spleen and liver. Also found in promyelocytic leukemia HL- 60 cells, chronic myelogenous leukemia K562 cells, Burkitt's lymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not detected in HeLa S3, Molt-4, A549 and G431 cells.
-1- SIMILARITY: CONTAINS I CARD DOMAIN.
-1- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS I GUANYLATE KINASE-LIKE DOMAIN.
-1- FROSITE, Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARA_HUMAN STANDARD; PRT; 1032 AA.
09BWT7; 09UGR5; 09Y3H0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGT 59
                      Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK. Stimulates the phosphorylation of Bcl10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                           phosphorylation of Bc110. 
 -1- SUBUNIT: CARD11 and Bc110 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 103 CARD.
123 442 COILED COIL (POTENTIAL).
673 748 PDZ.
966 1133 GUNYLATE KINASE.
808 808 P -> L (IN REF. 2).
1147 AA; 132641 MW; 913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS500856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PD2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.8%; Score 146; DB 1; 46.5%; Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.5%; Preu. ....
                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:16393; CARDII.'
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                       EMBL; AF322641; AAG53402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 46.5
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|||||| |
825 IPSYSRAQQLL 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 IPNYSRAQQQL 70

 (Carma 3).
 CARD10 OR CARMA3.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
           ERRATUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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MEDLINE-2122939; Pubbed-1125944;

Ranguline-2122939; Pubbed-1125944;

Ranguline-2122939; Pubbed-1125944;

Ranguline-2122939; Pubbed-1125944;

Ranguline-2122956; Pubbed-1125949; Pubbed-112509; Pubbed-11
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ZO3_MOUSE
                                                                                                                                                         SEQUENCE
                                                                                                                                                                         Query Match
                                                                                                                       Coiled
                                                                                                                                       DOMAIN
                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                755
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Ω
                                                                                                                                                                                                                                                              Dp
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
        CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                   2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam or SMART.
CAUTION: Ref.4 sequence differs from that shown due to various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                 Length 1032;
                                                                                                                                                                                                                     Q -> R (IN REF. 4).
K -> KQ (IN REF. 4; CAB63075).
R -> L (IN REF. 4).
                                                                                                                                                                                                                                                                                 29; Indels
                                                                                                                                                                                                                                      > L (IN REF. 4).
8377319AB82A0949 CRC64;
                                                                                                                                                                                           CARD.
COILED COIL (POTENTIAL).
POLY-SER.
                                                                                                                                                                                                                                                                30.1%; Score 116; DB 1;
40.0%; Pred. No. 1.6e-06;
tive 11; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1021 AA
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                            EMBL, AY028896; AAK26165.1; -.
EMBL, AX032928; AAK54454.1; -.
EMBL; AL049851; CAB63075.1; ALT_SEQ.
EMBL, AL049851; CAB63076.1; ALT_SEQ.
EMBL, AL022315; CAB42832.1; ALT_SEQ.
PROSITE; PS50209; CARD; 1.
                                            gene identification problems.
                                                                                                                                                                                                                                               115946 MW;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                            1115
456
574
289
917
932
                                                                                                                                                                                          23 11
138 45
567 57
289 26
917 91
932 AA;
                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                     PNYSRAQOOL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1) (Bimpl).
CARD10 OR BIMP1.
                                                                                                                                                                                    Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                               CARA_MOUSE
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
CARA_MOUSE
                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                  q
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-
like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DSFYIRVNLAMEGRAKGE-LQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAAHGTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.5%; Score 106; DB 1; Length 1021; 37.1%; Pred. No. 2.7e-05; Live 12; Mismatches 30; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                           65 POLY-SER.
114413 MW; 4811A09BDB8F792C CRC64;
                                                                                                                                                                                                                                                                                                                                                                            CARD. COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P31016; 1BFE.
MGD; MGI:1351650; Tjp3.
InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
MEDLINE=20069797; PubMed=10601346;
                                                                                                                                                                                                                                                                                              EMBL; AF363456; AAK60136.1; -.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF157006; AAF24175.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similaricy
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            115
450
565
                                                                                                                                                                                                                                                                                                                                                                                                                           558 56
1021 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| |||| ||
|PNYQRAQQLL 764
                            like domain. Bu
Pfam or SMART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PNYSRAQQQL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       coil.
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Wed Jan 22 10:56:43 2003

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3est Local Similarity
4atches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| :||:|
574 IPNKNRAEQ 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                            PF00595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TJP2 OR ZO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZOZ_CANFA
Q95168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tight
                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZOZ_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells is identical to 20-1, a tight junction-associated protein in epithelial cells: cDMA cloning and immunoelectron microscopy.";

J. Cell Biol. 121:491-502(1993).

FOUCTION: THE N-TETMINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL REQUIRED FOR TIGHT JUNCTION ASSEMBLY, WHILE THE C-TERMINAL MAY HAVE SPECIFIC PROPERTIES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN MIGHT BE INVOLVED IN STRABILIZING JUNCTIONS.

SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND ZO-3.

SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE CYPOPLASMIC SIDE.

MOVEMENT OF ZO-1 FROM THE CYTOPLASM TO MEMBRANE IS AN EARLY EVENT OCCURRING CONCURRENTLY WITH CELL-CELL CONTACT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh M., Nagafuchi A., Yonemura S., Yasuda-Kitani T., Tsukita S.,
Tsukita S.;
"The 220-kD protein colocalizing with cadherins in non-epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1fight junction protein ZO-1 (Zonula occludens 1 protein) (Zona cocludens 1 protein) (Tight junction protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                  Length 905;
                                                                                                                                                                                                                                                                                                           SH3.
GUANYLATE KINASE.
B787BA1592661FEE CRC64;
               InterPro; IPR001452; SH3.
Pfam; PF00595; PD2; 3.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM0072; GuKc; 1.
SMART; SM00328; PD2; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS50055; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50002; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 1;
Pred. No. 3.2e-05;
8; Mismatches 29
                                                                                                                                                                                                                              Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 11 93 PDZ 1.
DOMAIN 187 264 PDZ 2.
DOMAIN 368 434 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93252986; PubMed=8486731;
                                                                                                                                                                                                                                                                                                                                                        99324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                27.28;
37.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||| |||:|
522 DLREQERGVIPNOSRAEQ 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 -----HGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 37.28
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                  93
264
434
540
754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                         368
467
554
7
905 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZO1_MOUSE
P39447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR RODER DR 
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 GDSFYIRTHFEYEKESPYGLSFNKGEVFRVVDTLYNGKLGSWLAIRIGKNHKE--VERGI 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94179414; PubMed=8132716;
Jesaitis L.A., Goodenough D.A.;
"Molecular characterization and tissue distribution of ZO-2, a tight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96421547; Pubmed=8824195;
MEDLINE=96421547; Pubmed=8824195;
MEDLINE=96421547; Pubmed=8824195;
MEDLINE=96421547; Pubmed=8824195;
MEDLINE=96421547; Pubmed=8824195;
MEDLINE=9642154; Sequence of an alternatively spliced region.";
MEDLINE=96421543723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Čhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102.5; DB 1; Length 1745; Pred. No. 0.00013; 9; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annobtation update)
115-JUN tiunction protein 20-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C3DA2C0A9F411F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00856; GUANYLATE_KINASE_1; PROSITE; PS50052; GUANYLATE_KINASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO
                                                                                                                               PIR; A46431; A46431.
HSSP; P31016; 1BE9.
MGD; MGI:98759; Tjp1.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR0019696; ZUS.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                           PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194710 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               junction; SH3 domain;
                                                                                                            EMBL; D14340; BAA03274.1; -
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00791; ZU5; 1.
SMART; SM0072; GkC; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50106; PDZ; 3
PROSITE; PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1242 124
1424 143
1745 AA;
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SEQUENCE FROM N.A. (ISOFORM A1).

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RANGE BERKER RESERVED BY SERVED BY S
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                                                                                                                                                   PRODUCED BY ALLEARMAIN.
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANVLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Cell Biol. 124:949-961(1994).
-!- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
-!- SUBUNIT: INTERACTS WITH OCCLUDIN.
-!- SUBCELLULAR LOCATION: PERTPHERAL MEMBRANE. CYTOPLASMIC SIDE.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Membrane; Alternative splicing. PDZ 1. PDZ 2. PDZ 3.
junction protein homologous to ZO-1 and the Drosophila discs-large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202_HUMAN STANDARD; PRT; 1190 AA.
Q9UDY2; Q15883; Q9UDX1; Q9UDY0; Q99839;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein Z0-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein)
Typ2 OR Z02 OR X104.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; 45AB836BBDDB1226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 1; Le
Pred. No. 0.00013;
7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.00
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY -GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PP00018; SH3, 1.
Pfam; PP000595; PDZ, 3.
Pfam; PF00625; Guanylate_kin; 1.
SNART; SM00722 (GuKc, 1.
SNART; SM00328; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L27152; AAC37332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tight junction; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 39.1
les 27; Conservative
                          tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          860
1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| |||:|
643 IPNKSRAEQ 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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C. -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A1 (SHOWN HERE), C1, A2 AND C2;

ARE PRODUCED BY ALTERNATIVE SPLICING AND ALTERNATIVE INITIATION.

C. -!- TISSUE SPECIFICITY: THIS PROTEIN IS FOUND IN EPITHELIAL CELL

JUNCTIONS. ISOFORM A1 IS ABUNDANT IN THE HEART AND BRAIN WHEREAS

C. ISOFORM C1 IS EXPRESSED AT HIGH LEWEL IN THE KIDNEY, PANCREAS,

HEART AND PLACENTA. IN BRAIN AND SKELETAL MUSCLE, ONLY ISOFORM A1

IS DETECTABLE. ISOFORM C1 IS FOUND IN NORMAL AS WELL AS IN MOST

ON NORMAL TISSUE.

IN NORMAL TISSUE.

C. -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.

C. -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

C. -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.

C. -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.

C. -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION 1086

ONWARD DUE TO A FRAMESHIFT.
                                                                               Duclos F., Rodius F., Wrogemann K., Mandel J.L., Koenig M.; "The Friedrich ataxia region: characterization of two novel genes and reduction of the critical region to 300 kb."; Hum. Mol. Genet. 3:909-914(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlenski A., Ketels K.V., Korovaitseva G.I., Talamonti M.S., Oyasu R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarpelli D.G.; "Organization and expression of the human zo-2 gene (tjp-2) in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlenski A., Ketels K.V., Engeriser J.L., Talamonti M.S., Tsao M.-S., Koutnikova H., Oyasu R., Scarpelli D.G.; "Zo-2 gene alternative promoters in normal and neoplastic human pancreatic duct cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Aortic smooth muscle;
Adams L.D., Werny I., Schwartz S.M.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
-!- SUBBUNIT: INTERACTS WITH OCCUDIN.
-!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE, CYTOPLASMIC SIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99287578; PubMed=10360833; Chlenski A., Ketels K.V., Tsao M.-S., Talamonti M.S., Anderson M.R., Oyasu R., Scarpelli D.G.; "Tight junction protein Zo-2 is differentially expressed in normal pancreatic ducts compared to human pancreatic adenocarcinoma."; Int. J. Cancer 82:137-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-104 FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A. (ISOFORMS A1 AND C1).
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS A1; C1; A2 AND C2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 1493:319-324(2000).
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EMBL; AF177533; AAD20387.2; -.
EMBL; AF043195; AAD20387.2; JOINED.
EMBL; AF043196; AAD20387.2; JOINED.
EMBL; AF043197; AAD20387.2; JOINED.
EMBL; AF17518; AAD20387.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99426875; PubMed=10495427;
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20472048; PubMed=11018256;
FISSUE=Brain;
MEDLINE=95038744; PubMed=7951235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Int. J. Cancer 83:349-358(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1047-1167 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplastic tissues.
                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50106; PDZ; 3.
Tight junction; SH3; 1.
Tight junction; SH3 domain; Repeat; Membrane; Alternative splicing; CHAIN 1 1190 TIGHT JUNCTION PROTEIN ZO-2, ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6 X CBA;
MBDLINE=99150392; PubMed=10026224;
Itoh M., Morita K., Tsukita S.;
"Characterization of 20-2 as a MAGUK family member associated with
tight as well as adherens junctions with a binding affinity to
                                                                                                                                                                                A1/A2.
TIGHT JUNCTION PROTEIN ZO-2, ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein) (Zona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 1; Length 1190;
Pred. No. 0.00018;
7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM A2/C2).

I -> Y (IN REF. 1).

P -> S (IN REF. 1).

FEN -> SFT (IN REF. 1).

K -> N (IN REF. 1).

N -> D (IN REF. 1).

O -> H (IN REF. 1).

P -> S (IN REF. 1).

P -> S (IN REF. 1).

P -> S (IN REF. 1).

S -> N (IN REF. 5).

GSYG -> RSFC (IN REF. 5).

EYR -> INS (IN REF. 5).

EYR -> INS (IN REF. 5).
                                                                                                                                                                                                        C1/C2.
FOR ISOFORMS C1/C2.
PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-2 (Zonula occludens 2
occludens 2 protein) (Tight junction protein 2).
TJP2 OR ZO2.
                                                                                                                                                                                                                                                                                            GUANYLATE KINASE. POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1167 AA
Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; Gukc; 1.
SMART; SM00328; PDZ; 3.
SMART; SM00326; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 39.1
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 IPNKSRAEQ 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 IPNYSRAQQ 68
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SEQUENCE
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202_MOUSE
10 202_M
DT 16-0C
DT 16-0C
DT 16-0C
DT 15-JU
DE Tight
DE CCIU
GN CCIU
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MEDLINE=93361541; PubMed=8395056;
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SEQUENCE
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                      SO THE FEFFE FEFFE BRAND BRAND
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                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
occludin and alpha catenin.";
J. Biol. Chem. 274:5981-5986(1999).
-!- FUNCTION: PLAYS A ROLE IN TIGHT JUNCTIONS AND ADHERENS JUNCTIONS.
-!- SUBUNIT: INTERACTS WITH OCCLUDIN.
-!- SUBULILIAR LOCATION: PREIPHERAL MEMBRANE. CYTOPLASMIC SIDE.
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOWAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tight junction protein 20-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DrackTrio, Trockto, 200.

Pfam; PF0018; 873; 1.

Pfam; PF0018; 873; 1.

SMART; SM00072; GuKC; 1.

SMART; SM00026; PDZ; 3.

SMART; SM00326; BDZ; 3.

SMART; SM00326; GUANYLATE_KINASE_1; FALSE_NEG.

PROSITE: PS50052; GUANYLATE_KINASE_2; 1.

PROSITE: PS50005; PDZ; 3.

PROSITE: PS50005; BDZ; 3.

Tight junction; SH3 domain; Repeat; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 1; 1
Pred. No. 0.00023;
7; Mismatches 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3.
GUANYLATE KINASE.
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01-07T-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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MGD; MGI:1341872; Tjp2.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
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PDZ 2.
PDZ 3.
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39.1%;
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Best Local Similarity
Matches 27; Conserv
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639 IPNKSRAEQ 647
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TJP1 OR ZO1.
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Q07157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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201_HUMAN
ID 201_H
AC 20715
DT 01-0C
DT 01-0C
DT 15-JU
DE Tight
DE OCCIU
GN HOMO
OC MAMMAM
OCC MAMMAM
OCC NOCBI
RN [1]
RR [1]
RR SEQUE
RC TISSU
                      SOLUTION NEW YEAR A SOLUTI
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,
                                                     ATTENDED FOR THE ACAC SECTION OF SEPTIAL DEPOSOPHILA

"THE Light junction protein 20-1 is homologous to the Drosophila

RT discs-large tumor suppressor protein of septate junctions.";

Proc. Natl. Acad. Sci. U.S.A. 90.7834-7838(1993).

1. FUNCTION: THE N-TERMINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL

REQUIRED FOR TIGHT JUNCTION ASSEMBLY, WHILE THE C-TERMINAL MAY

HAVE SPECIFIC PROPERTIES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN

MIGHT BE INVOLVED IN STABILIZING JUNCTIONS.

1. SUBBUILT: INTERACTS WITH OCCLUDIN AND ZO-3.

1. SUBGELLULAR LOCATION: PERIPHERAL MEMBRANE. CYTOPLASMIC SIDE.

MOVEMBRY OF ZO-1 FROW THE CYTOPLASM IS AN EARLY EVENT

COCCURRING CONCURRENTLY WITH CELL-CELL CONTACT.

1. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1. TISSUE SPECIFICITY: THE ALPHA-CONTAINING ISOFORM IS FOUND BOTH IN

EPITHELIAL CELL JUNCTIONS: THE SHORT ISOFORM IS FOUND BOTH IN

EPITHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COF RENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS

COFFICE AND THE HIGHLY SPECIALIZED SPECIALIZED EPITHELIAL JUNCTIONS

COFFICE AND THE HIGHLY SPECIALIZED SPECI
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-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-: SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-: SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tight junction; SH3 domain; Alternative splicing; Repeat; Membrane; Phosphorylation.
Willott E., Balda M.S., Fanning A.S., Jameson B., van Itallie C.,
Anderson J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
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Pred. No. 0.00042;
9; Mismatches 32; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SHORT ISOFORM). W; 508D01B7A0814FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG-
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3.
GUANYLATE KINASE.
POLY-PRO.
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PDZ 2.
PDZ 3.
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InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000906; 2U5.
Pfan; PP00595; PD2; 3.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00791; 2U5; 1.
SWART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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36.2%;
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Best Local Similarity 36.2
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P31016; 1BFE.
Genew; HGNC:11827; TJP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED.
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SMART; SM00326; SH3; 1.
SMART; SM00218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572
782
1236
1420
989
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1736 AA;
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Wed Jan 22 10:56:43 2003

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Brower A., Gordon L., Diasa J., Ramirez M.,
Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
A Avila J., Liu S., Attix C., Andreise T., Trankheim M.,
A Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,
A Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D.,
A Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
r serine protease gene cluster.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
--- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
--- SIMILARITY: CONTAINS 1 SH3 DOMAINS.
--- SIMILARITY: CONTAINS 1 GANNYLATE KINASE-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 1 GANNYLATE KINASE-LIKE DOMAIN.
--- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                              Homo saplens (Human).
Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona cocludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 GUANYLATE KINASE.
102800 MW; 680298CFD0615B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P31016; 1BFE.

Genew; HGNC:11829; TJP3.

InterPro; IPR0001478; PD2.

InterPro; IPR001478; PD2.

InterPro; IPR001478; PD2.

InterPro; IPR001452; SH3.

Pfam; PF00655; Guanylate_kin; 1.

SMART; SM00072; Guanylate_kin; 1.

SMART; SM00228; PD2; 3.

SMART; SM00228; PD2; 3.

PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.

PROSITE; PS500106; PD2; 3.

PROSITE; PS501006; PD2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 195 272 PDZ 2.
DOMAIN 394 460 PDZ 3.
DOMAIN 489 563 SH3.
                                                                                                                                                                                         933 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC005954; AAC72274.1; ALT_INIT.
                                                                                                                                                                                         STANDARD;
                                               ||| :||:|
562 IPNKNRAEQ 570
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Best Local Similarity
                    68
                    60 IPNYSRAQO
                                                                                                                                                                                         ZO3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROFEINS.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haskins J., Gu L., Wittchen E.S., Hibbard J., Stevenson B.R., "ZO-3, a novel member of the MAGUK protein family found at the tight junction, interacts with ZO-1 and occludin."; J. Cell Biol. 141:199-208(1998).
    Gaps
                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCG-----CWHAHRVNSYTMKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-3 (Zonula occludens 3 protein) (Zona occludens 3 protein) (Tight junction protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
  33; Indels
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8091D6132DB9F15D CRC64;
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Pred. No. 0.00064;
7; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS550052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Membrane
                                                                                                                                                                                                                                                                                                     898 AA
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  7; Mismatches
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MEDLINE-98198478; Pubmed-9531559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF023617; AAC39177.1; -. HSSP; P31016; 1BFE.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Ffam; PF00595; PDZ; 3.
Ffam; PF00625; Guanylate_kin; 1.
SMART; SM00128; Guanylate_kin; 1.
SMART; SM00128; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                     PRT;
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98414 MW;
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36.0%;
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28; Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                 Canis familiaris (Dog)
                                                                                                                                      68
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Best Local Similarity
                                                                                                                                      56 AHGTIPNYSRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                   ZO3_CANFA
O62683;
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Pred. No. 0.00038;
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38.4%;
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78183 MW; F50E6290E0B6EA12 CRC64;

686 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McKie N., Dando P.M., Rawlings N.D., Barrett A.J.; "Thimet oligopeptidase: similarity to 'soluble angiotensin II-binding protein' and some corrections to the published amino acid sequence of
  464 GDSFYIRTHFELEASPPSGLGFTRGDVFHVLDTLCPGPGPSGARGTHWLAVRMGRDLREQ 523
                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Thimet oligopeptidase (E. 3.4.L415) (Endo-oligopeptidase A)
(Endopeptidase 24.15) (PZ-peptidase) (Soluble metallo-endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Testis;
MEDLINE-91084500; PubMed-2261476;
Pierotti A., Dong K.-W., Glucksman M.J., Orlowski M., Roberts J.L.;
Molecular cloning and primary structure of rat testes
metalloendopeptidase EC 3.4.24.15.";
Biochemistry 29:10323-10329(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGRADATION.
CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF THE PHE-|-ALA BOND
IN SUBSTRATES CONTAINING -PHE-PHE-|-ALA-ALA-PHE- AND SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the rat testis enzyme.";
Biochem. J. 295:75-60(1993).
-!- FUNCTION: INVOLVED IN THE METABOLISM OF NEUROPEPTIDES UNDER 20
AMINO ACID RESIDUES LONG. INVOLVED IN CYTOPLASMIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: BINDS 1 ZINC ION.
-:- SUBUNIT: MONOMER.
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE TESTIS.
IT IS ALSO FOUND IN THE LIVER, LUNG AND KIDNEY.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CATALYTIC) (BY SIMILARITY).
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(BY
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BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC) (
                                                                                                                                                                                                                                686 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01432; Peptidase_M3; 1. PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94029935; PubMed-8216239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M61142; AAA41586.1; -.
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                --ERGIIPNOSRAEQ 536
                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A36165; HYRTTH.
PIR; S38760; S38760.
MEROPS; M03.001; -.
                                                                     54 TAAHGTIPNYSRAQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473
476
479
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                                                                                                                                                                                                                                MEPD_RAT
P24155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENTE FROM N.A.

MEDLINE-2070548: Pubbled=10603080;
Suprenant K.A., Tuxhorn J.A., Daggett M.A.F., Ahrens D.P.,
Suprenant K.A., Palange J.M., VanWinkle C.E., Livingston B.T.;
Hostetler A., Palange J.M., VanWinkle C.E., Livingston B.T.;
"Conservation of the WD-repeat, microtubule-binding protein, EMAP, in
sea urchins, humans, and the nematode C. elegans.";
Dev. Genes Evol. 210:2-10(2000).
-!- FUNCTION: May modify the assembly dynamics of microtubules, such
that microtubules are slightly longer, but more dynamic.
-!- SIMILARITY: CONTAINS 9 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE EMAP FAMILY OF WD-REPEAT PROTEINS.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                    Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                          Gaps
                                                                                2 DSFYIRVNL----AMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHAHRVNSYTMKDTAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                        .;
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  Length 686;
                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
77 KDa echinoderm microtubule-associated protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                        Indels
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                                      21:
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  DB 1;
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16.5%; Score 63.5; Di
30.0%; Pred. No. 3.4;
                                                                                                                                                                                                                           664 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00400; WD40; 7.
Pfam; PF00411, HELP: 1.
SMART; SM00320; WD40; 1.
PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50082; WD_REPEATS_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%; Score 62.5; 30.1%; Pred. No. 4.
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                                        14;
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InterPro; IPR005108; HELP.
InterPro; IPR001689; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73423 MW;
                                        Conservative
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                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664 AA;
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les 22; Conserv
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7654;
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218
2265
3307
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Q9Y1C1;
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Matches
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Dp O D

42 -HAHRVNSYTMKD 53 | | | : |:| 423 QHTQRWNKF-MED 434

Search completed: January 22, 2003, 08:53:37 Job time : 4.72849 secs

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Q94791 drosophila Q94792 drosophila Q95479 drosophila Q95420 drosophila Q95420 drosophila Q94470 arabidopsis Q94470 arabidopsis Q94417 pseudomonas Q9417 pseudomonas Q9527 mus musculu Q99915 drosophila Q96041 drosophila Q96041 drosophila Q94091 drosophila Q94091 drosophila Q94091 drosophila

Q8yri3 anabaena sp Q91xv2 rattus norv

Minimum DB Maximum DB

Database

Searched:

Q9epx1 mus musculu

0944u0 oryza sativ 09f7t9 streptomyce 09s0r8 streptomyce

091wjl mus musculu Q8v520 monkeypox v

095m07 bos taurus 08ww07 homo sapien 060260 homo sapien

homo sapien

091xv1 rattus norv

OM protein

Run on:

Sequence:

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1 GDSFYIRVNLAMEGRAKG-ELQVHCNEVLHVTDTMFQGGGGWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.6%; Score 145; DB 4; Length 1171;
46.5%; Pred. No. 1.2e-10;
tive 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1171 AA; 134966 MW; FAS67ABBC8A703FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AK074049; BAB84875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1171 AA
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849 IPSYSRAQQLL 859
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nes 33; Conserv
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TISSUE=SPLEEN;
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Q9bkl2 hydra atten
Q20398 caenorhabdi
Q92199 mus musculu
O97758 canis famil
P70625 rattus nory
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gallus gall
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0960n4 drosophila
094880 drosophila
090hk4 drosophila
090kb4 homo sapien
09vkg drosophila
09vkg homo sapien
09ykg homo sapien
08tdm7 homo sapien
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homo sapien
homo sapien
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Q9nf04 caenorhabdi
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                                                                                                                                                                    (without alignments)
1321.544 Million cell updates/sec
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                                                                                                                                            January 22, 2003, 08:49:36; Search time 10.914 Seconds
                                                                                                                                                                                                                                                                      1 GDSFYIRVNLAMEGRAKGEL.........MKDTAAHGTIPNYSRAQQQL 70
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                                                                                                                                                                                                                                                                                                                                                                                                                         671580
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             671580 segs, 206047115 residues
                                                                                                                                                                                                                    US-09-767-215-2_COPY_676_745
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                                                                                                      - protein search, using sw model
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Q9NF04
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Q9VHK4
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Q9VKG8
Q9UE73
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q8TDM7
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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seq length: 200000000
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116.1
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102.5
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97.5
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96.5
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No. Result

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SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00226; SH3; 1.
SMART; SM00316; SH3; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
SEQUENCE 1695 AA; 190878 MW; AE0E7D0900
                        Guanylate_kin
                                                                  InterPro; IPR001452; SH3.
InterPro; IPR001905; ZU5.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00755; PDZ; 3.
Pfam; PF00791; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.1%;
Best Local Similarity 41.7%;
Matches 30; Conservative 1
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RGVLPNKSRAEQ 831
                     InterPro; IPR000619;
InterPro; IPR001478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Les 25; Conserv
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HSSP; P29476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                             Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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MEDLINE-21025768, PubMed-11225567;

MEDLINE-21025768, PubMed-11225567;

"Molecular and biological characterization of a zonula occludens-1
"Molecular and biological characterization of a zonula occludens-1
homologue in Hydrax vulgaris, named HZO-1.";

Dev. 210:611-616(2000).

EMBL; AF230482; AAK28322.1;
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Bukaryota; Metazoa; Cnidarla; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.8%; Score 126.5; DB 5; Length Best Local Similarity 42.5%; Pred. No. 4.3e-08; Matches 31; Conservative 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50052; GGANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
SEQUENCE 1257 AA; 139392 MW; 617E729417136819 CRC64;
                                                                                                                                                                                                                                                                                                                                     Sulston J.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tight junction protein ZO-1.
                                                                             Last sequence update)
Last annotation update)
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  PRT; 1257 AA
                                                     Created)
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Interpro; IPR001478; PDZ.
Interpro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00655; Guanylate_kin; 1. Pfam; PF00791; 2U5; 1. SMART; SM00728; GuKc; 1. SMART; SM00228; PD2; 3. SMART; SM00326; SH3; 1. SMART; SM00218; 2U5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL132879; CAB60860.2;
HSSP; Q12923; 3PDZ.
                                             01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000906; ZUS
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  PRELIMINARY;
                                                                             1-OCT-2000 (TrEMBLrel.
1-JUN-2002 (TrEMBLrel.
                                                                                                                                                  Y105E8C.B.
Caenorhabditis elegans
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550 VKGVIPNQATAEQ 562
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                                                                                                  01-JUN-2002 (Tremb. Y105E8C.b protein.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BKL2
Q9BKL2;
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NCBI_TaxID=6239;
                                                                                                   Gaps
                                                                                                                                               1 GDSFYIRVNLAMEGRAK-GELQVHCNEVLHVTDTMFQG-CGCWHAHRV--NSYTMKDTAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                              8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL: 268298; CAA92607.1; ...
InterPro; IPR001478; PDZ.
Pfam, PF00595; PDZ.
SAMAT; SM00722; GUKC; 1.
SMART; SM00228; PDZ; 3.
PROSITE; PSS5005; GUANYLATE_KINASE_2; 1.
PROSITE; PSS5005; GUANYLATE_XINASE_2; 1.
SEQUENCE 1034 AA; 116053 MW; 7E29646264FCD5BC CRC64;
                                                   Length 1695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for
190878 MW; AE0E7D09007316F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                              Score 116; DB 5; L
Pred. No. 1.7e-06;
1; Mismatches 23;
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35.2%; Pred. No. 2.5e-05;
live 12; Mismatches 31
                                                                                                 11; Mismatches
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InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
InterPro; IPR000906; ZU5.
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P70625
    DR KW KW SO OR SO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.2%; Score 105; DB 11; Length 904; Best Local Similarity 37.2%; Pred. No. 2.4e-05; Matches 29; Conservative 8; Mismatches 29; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RMED: MGJ 11315650; Tip3.
RMCD: MGI:1131650; Tip3.
RMCD: MGI:1131650; Tip3.
RMCD: RMCD: PR000619; Guanylate_kin.
RMCD: RMCD: PR001478; PDZ.
RMCD: PR00555; PDZ. 3.
RMCD: PR01597; ZONOCCLUDNS.
RMINTS; PR01697; ZONOCCLUDNS.
RMINTS; PR01600; ZONOCCLUDNS.
RMINTS; PR01600; ZONOCCLUDNS.
RMINTS; PR01600; ZONOCCLUDNS.
RMCSTTE; PS50052; GANNYLATE_KINASE_2; 1.
RMCSTTE; PS50062; GANNYLATE_KINASE_2; 1.
RMCSTTE; PS50062; GANNYLATE_KINASE_2; 1.
SEQUENCE 904 AA; 99169 MW; A4D9CSBAEEC485CC CRC64;
                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to tight junction protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                           904 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exp. Cell Res. 248:97-109(1999).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U55935; AAD11529.1; --
HSSP; P31016; 1BE9.
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BREED: COCKER SPANIEL;
MEDLINE=99196918; PubMed=10094817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ||| |||:|
521 DLREQERGVIPNOSRAEQ 538
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                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
       ||:: | :
811 IPSSTTVYQAI 821
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZO1-MDCK
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                                                                                             RESULT 5
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[1]
SEQUENCE FROM N.A.
MEDLINE=20027749; PubMed=10559001;
MEDLINE=20027749; PubMed=10559001;
MAGHNE D.D., Lemire J.M., Schwartz S.M.;
A systematic analysis of 40 random genes in cultured vascular smooth muscle subtypes reveals a heterogeneity of gene expression and identifities the tight junction gene zonula occludens 2 as a marker of epithelioid 'pup' smooth muscle cells and a participant in carotid neointimal formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.6%; Score 102.5; DB 6; Length 1769; Best Local Similarity 37.7%; Pred. No. 0.00012; Matches 26; Conservative 9; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;
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-!- STMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL. 9175916; AA446979.1; -.
HSSP; P31016; AB446979.1; -.
HSSP; P31016; AB446979.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR01597; ZONOCCLUDNS.
PRINTS; PR01599; ZONOCCLUDNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70625; P97625;
P10625 (TrEMBLrel. 02, Created)
01-JNN-2002 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1. SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zonula occludens 2 protein (Fragment)
Pfam; PP00625; Guanylate_kin; 1. Pfam; PP00595; PD2; 3. Pfam; PP00189; SH3; 1. Pfam; PP00791; 2U5; 1. PRINTS; PR01597; ZONOCCLUDNS. PRINTS; PR01609; ZONOCCLUDNS. PRINTS; PR01609; ZONOCCLUDNS. SMART; SM00725; GuKc; 1. SMART; SM00228; PD2; 3. SMART; SM00218; ZU5; 1.
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SMART; SM00228; PDZ; 1.
SMART; SM00326; SH3; 1.
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573 IPNKNRAEQ 581
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Query Match
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        RESULT 9
Q960N4
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                231 GDSFFIRSHFECEKETPQSLAFTRGEVFRVVDTLYDGKLGHWLAVRIGNELEK----GL 285
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                  Collins J.R., Rizzolo L.J.;
Protein-binding domains of the tight junction protein, ZO-2, are highly conserved between avian and mammalian species.";
Biochem. Biophys. Res. Commun. 252:617-622(1998).
EMBL; AROBSI84, AAC95469.1;
EMBL; AF085184; AAC95469.1;
HSSP; P31016; 1BE9
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9
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                                                 Query Match 25.9%; Score 100; DB 11; Length 813; Best Local Similarity 39.1%; Pred. No. 0.0001; Matches 27; Conservative 7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1163 AA; 130668 MW; 3639431A560B1D4E CRC64;
                             30EA78F19DE9C852 CRC64;
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                   Created)
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PRINTS: PR01599; ZONOCCLUDNS2.
PRINTS: PR01600; ZONOCCLUDNS3.
SMART; SM00072; Gukc; 1.
SMART; SM00328; PD2; 3.
SMART; SM00326; SH3; 1.
                           90776 MW;
                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21, Tight junction protein.
PROSITE; PS50002; SH3; 1
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                           813 AA;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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| 628 IPNRSRAEQ 636
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286 IPNKSRAEQ 294
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                                                                                                                                       60 IPNYSRAQQ 68
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                                                                                                                                                                                                                                                                                                                                                               TISSUE-RETINA;
            SH3 domain.
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SEQUENCE
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Charin H., Li P., Liao G., Miranda A., Mungail C.J.,
Nunco J., Paragas V., Paragas 
                                                                                                                                                                                                                                                                  PYD OR CG9763.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=96312452; PubMed=8698238;
MEDLINE=96312452; PubMed=8698238;
Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A., Kondo K., Miyake T., Ueda R.;
Tondo K., Miyake T., Ueda R.;
"The Drosophila tamou gene, a component of the activating pathway of extramacrochaetae expression, encodes a protein homologous to mammalian cell-cell junction-associated protein ZO-1.";
Genes Dev. 10:1783-1795(1996).
ENBL; D83477; BAA11923.1; -.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.3%; Score 97.5; DB 5;
31.9%; Pred. No. 0.00028;
iive 13; Mismatches 31;
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                                                                                                            Created)
                                                                                                       01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
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PRELIMINARY;
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RESULT 12
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RAY ADGUBINE FROM N.A.

RADILINE-20196006; PubMed-10731132;

RADILINE R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RADILINE R.C., Rogers Y.-H.C., Blazej, K.G., Champe M., Pfeiffer B.D.,

RADILINE, Apdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RADILINE, Apdayani A., Burler H., Cadieu E., Center A., Chandra I.,

RADILINE, R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADILINE, R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADILIS R.C., Rowing S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADILIS R.C., Rogers R., Danks C., Rerrac C., Ferriera S., Fleischmann W.,

RADILINE, R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADILINE, R.C., Rongelista C.C., Ferrac C., Ferriera S., Fleischmann W.,

RADILINE, R.C., Howland T.J., Weil M.-H., Ibegwam C.,

ADAIL M., Kalush F., Karpen G.H., Ke Z., Kennison J. A., Ketchum K.A.,

ADAIL M., Kalush F., Karpen G.H., Ke Z., Kennison D.,

ALLINE, Mattel B., McIntcosh T.C., McLeod M.P., McPherson D.,

ALLINE, Mattel B., McIntcosh T.C., McLeod M.P., McPherson D.,

ALLINE, Mattel B., McIntcosh T.C., McLeod M.P., McPherson D.,

ALLINE, Mattel B., McIntcosh T.C., McLeod W.P., McPherson D.,

ADAIL M., Mallshing N.V., Mobarry C., Scheeler F., Shen H.,

RADILINE, Radilland R.S., Pan S., Pollari J., Purl V., Resse M.G.,

RADILINE, Radich R.S., Mixon K., Sanders M.P., Shen H.,

RADILINE, R. Reinerton G.S., Pan S., Pollari J., Purl V., Resse M.G.,

RADILINE, R. Reinerton R.S., Suppson M., Shupski M.P., Shith T.,
                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neotera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                              1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                               Query Match 25.3%; Score 97.5; DB 5; Length 1367; Best Local Similarity 31.9%; Pred. No. 0.00042; Matches 22; Conservative 13; Mismatches 31; Indels 3;
                                                                                                                                                                                               148347 MW; 571C4566C6B6BBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1445 AA.
           Interpro; IPR000619; Guanylate_kin.
Interpro; IPR001478; PDZ.
Interpro; IPR001478; PDZ.
Interpro; IPR001452; SH3.
Pfam; PF00655; DDZ, 2.
SMART; SM00072; GuKc; 1.
SMART; SM00028; PDZ, 3.
SMART; SM00328; PDZ, 3.
SMART; SM00326; SH3; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
FlyBase; FBgn0003177; pyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                 1367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      ||| |||:
556 IPNKSRAEE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               60 IPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYD protein.
PYD OR CG9763.
                                                                                                                                                                                               SEQUENCE
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.
M. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.G.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
R. Embl. AE003680; AAF54300.1; -.
R. Fibbase; FSP00001377; pyd.
R. Fibrerpro; IPR001478; pbg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 GDSFHIKTHFHCDNPSKGEMAFKAGDVFRVIDTLHNGVVGSWQVLKIGRGHQE--MQRGV 555
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TISGUENCE FROM N.A.

TISGUENCE TO, AND MINLY HEAD;

TISGUENCE T., OLT T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Isogai T., OLT T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Aritam T., Namura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

A Aritam N., Nabackura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

A Aritam N., Nabamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human CDNA sequencing project.";

L Submitted (MAY 2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; AK027292: BAB55020.1;

InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R Pfam: PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQG-CGCWHAHRVNSYTMKDTAAHGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14386 fis, clone HEMBA1002417, moderately similar to TIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156723 MW; A5675FB66676A40E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 97.5; DB 5; 31.9%; Pred. No. 0.00045; ive 13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 6. SEQUENCE 1445 AA; 156723 MW; A5675FBé
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PRRINTS; PR01600; ZONOCCLUDNS3.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00595; PDZ; 2.
Pfam; PP00791; ZU5; 1.
SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00328; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.9%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000906; ZU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     junction protein ZO-1. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001452;
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Ra Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Ra Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Ra Goorge R.A., Lewis S.E., Richards S., Ashbunner. M., Henderson S.N.,
Rautcon G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.H.C., Blazej R.G., Change M., Miklos G.L.G.,
Randon R.C., Rogers Y.H.C., Blazej R.G., Change M., Pfeiffer B.D.,
Randon R.C., Rasandal A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballaw R.M., Basu A. Baxendala D., Baytaktaroju L., Beasley E.M.,
Beeson K.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ra Burtis K.C., Busam D.A., Bulle C., Davenport L.B., Davies P.M.,
Ra Burtis K.C., Busam D.A., Bulle C., Davenport L.B., Davies P.M.,
Ra Cherry J.M., Cawley S., Dallake C., Davenport L.B., Davies P.M.,
Ra Cherry J.M., Cawley S., Dallake C., Davenport L.B., Davies P.M.,
Ra Clodek A., Gong F., Gorrell J. H., Gallar W., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Ra Glodek A., Gong F., Gorrell J. H., Gu Z., Gelbart W.M., Glasser K.,
Ra Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Liu X., Mattei B., McIntosh T.C., McIeod M.P., Morherson D.L.
Amerkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Randlar M., Palush R.A., Nixon K., Morris J., Moshrefi A.,
Shue B.C., Siden-Kiamos I., Simpson M., Sturon R.,
Shue B.C., Siden-Kiamos I., Simpson M., Sturong R., Sun E.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K.G., Wu D., Yang S., Zhoo Q., A.,
Walliams S.M., Woodage T., Worley K.G., Wu D., Yang S., Zhoo Q., Shon R.,
Rance B.C., Shorn S.W., Rubin G.M., Venter E., Wang K.,
Rance B.C., Shorn S.W., Rubin G.M., Venter E., Wang K.,
Rance B.C., Shorn S., Worley K.G., Wu D., Yang S., Zhon Q., Shorn S.,
Rance B.C., Shorn S., Worley R.W., Rubin G.M., Venter E.,
Rance B.C., Shorn S., Rance B.C., Shorn S.,
Rance
                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                             1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGCGCWHA---HRVNSYTMKD--TA 55
                                                                              ŝ
                                           Score 96.5; DB 4; Length 548;
Pred. No. 0.00019;
7; Mismatches 33; Indels 5
PROSITE; PS50002; SH3; 1.
SEQUENCE 548 Aa; 61005 MW; Alalecfde2627AC CRC64;
                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                              PRT; 1916 AA.
                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000).
                                               25.0%;
38.4%;
                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, CG6509 protein (LD32687p).
                                       Query Match
Best Local Similarity 38.4<sup>†</sup>
Matches 28; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                   164 ERGIIPNOSRAEO 176
                                                                                                                                                                       56 AHGTIPNYSRAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                                              RESULT 13
Q9VKG8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GDSFYIRVNLAMEGRA-KGELQVHCNEVLHVTDTMFQGC-GCWHAHRVNSYTMKDTAAH- 57
STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR003632; AAF53102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 95; DB 5; Length 191r
34.2%; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00228; PDZ; 4.
SMART; SM00326; SH3; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50052; PDZ; 4.
SEQUENCE 1916 AA; 209863 MW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 13, Last annotation update)
Discs large protein P-dlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 14; Mismatches
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SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 2.
PRART; SM00326; SH3; 1.
PROSITE: PS50052; GUANTLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR000619; Guanylate_kin.
Interpro: IPR001478; Pb2.
Interpro: IPR000408; Reg_chr_condens.
Interpro: IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                   Flybase, FBGn0032363, CG6509.
InterPro; IPR000619; Guanylate_Kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452, SH3.
Pfam; PF00595; PDZ, 3.
SMART; SM00072; GuKc; 1.
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Pfam; PF00595; PDZ; 2.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1644 KECGIIPSOMKVEEEL 1659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 26; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                HSSP; P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q9UE73
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5;
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Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GDSFYIRVNLAMEGRAKGELQVHCNEVLHVTDTMFQGC-GCWHAHRVNSYTMKDTAAHGT 59
                                                                                                       3; Gaps
                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998)

-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.

EMBL; AB011155; BAA25509.1; -.

HSSP; 012959; 1PDR.

InterPro; IPR001619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                       Homosapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.3%; Score 78.5; DB 4; Length 1281; Best Local Similarity 34.9%; Pred. No. 0.15; Matches 22; Conservative 10; Mismatches 28; Indels 3;
                                                                      Query Match 20.3%; Score 78.5; DB 4; Length 674; Best Local Similarity 34.9%; Pred. No. 0.069; Matches 22; Conservative 10; Mismatches 28; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1
SEQUENCE 1281 AA; 140286 MW; 4CC150D03F3ED8B9 CRC64;
                                           674 AA; 74892 MW; C4C006B0A4F7E8E8 CRC64;
                                                                                                                                                                                                                                                                                                            0374E3.
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-2002 (TrEMBLrel. 21, Last annotation update)
KIAAO583 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR000452; SH3.
Pfam; PP00625; Guanylate_kin; 1.
Pfam; PP00625; Guanylate_kin; 1.
Pfam; PP00625; BH3; 1.
Pfam; PP00018; SH3; 1.
PRINTS; PR00422; SH3DOMAIN.
SMART; SM00228; PDZ; 4.
SMART; SM00228; PDZ; 4.
PROSITE; PS50052; GUANYLATE_KINASE_2; 2.
PROSITE; PS50106; PDZ; 4.
PROSITE; PS50106; PDZ; 4.
PROSITE; PS50106; PDZ; 4.
PROSITE; PS50106; PDZ; 4.
PROSITE; PS00626; RCC1_2; UNKNOWN_1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                ||:
406 IPS 408
              PROSITE; PS5
SH3 domain.
SEQUENCE 6
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                                                                                                                                                                                             60 IPN 62
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b 1013 IPS 1015
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Search completed: January 22, 2003, 08:56:45 Job time : 13.914 secs

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January 22, 2003, 08:49:35; Search time 34.8857 Seconds (without alignments) 683.714 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SOMMAKIES		Description	Human caspase recr	Human predicted ca	Human caspase recr	Human polypeptide	Human polypeptide,	Human plakoglobin	Human caspase recr	Human P-dlg protei	Mouse quanylate ki	AA sequence (III)
	æ	ID	AAE07164	AAE07165	AAU01207	AAM38934	AAM93822	AAU73247	AAU01206	AAW72748	AAR93137	AAP70243
		DB	22	22	22	22	22	23	22	19	16	80
		Length	1004	1139	1147	350	746	1032	1032	674	198	197
		Query Match	100.0	95.1	26.1	18.9	18.9	18.9	18.2	13.8	13.4	13.1
		Score	930	884	242.5	175.5	175.5	175.5	169.5	128.5	124.5	121.5
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/note= "cAMP- and cGMP-dependent protein kinase ohosphorylation site"
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/note= "Casein kinase II phosphorylation site"
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2= "Casein kinase II phosphorylation site"
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:e= "Protein kinase C phosphorylation site"
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ce= "Casein kinase II phosphorylation
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.e= "Peroxisomal targetting signal"
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196..799
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/note= "N-glycosylation site"
602..605
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    note- "Casein Kinase II phosphorylation site"
'note- "Casein kinase II phosphorylation site"
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e- "Protein kinase C phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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e- "Casein kinase II phosphorylation site"
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.e- "Casein kinase II phosphorylation site"
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.e= "Protein kinase C phosphorylation site"
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107..310
//note= "Casein kinase II phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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466
e= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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121..123
/note= "Protein kinase C phosphorylation site"
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165..168
/note= "Casein kinase II phosphorylation site"
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221. 224
'note= "Casein kinase II phosphorylation site"
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e= "Protein kinase C phosphorylation site"
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                                           'note= "Protein kinase C phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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e= "Tyrosine kinase phosphorylation site"
                   /note= "Protein kinase C phosphorylation site"
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.e= "Tyrosine kinase phosphorylation site"
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.e= "Casein kinase II phosphorylation
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e= "Leucine zipper pattern"
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/note= "N-myristoylation site"
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516
2= "N-myristoylation site"
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te= "N-myristoylation site"
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ce= "N-myristoylation site"
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.979 .e= "Casein kinase II phosphorylation site" /note= "Protein kinase C phosphorylation site" /note= "N-myristoylation site" 1002..1004

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                                                      The present sequence is human caspase recruitment domain-14 (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind commodulators that modulates the ability of CARD-14 to of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of cancer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders because immune disorders (e.g., canomia, myelodysplastic syndromes), mycocardial infactions, strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling disorders and certain viral and bacterial infections.
regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                              VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
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                                                                                                                                                                                                                                                                                                 1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                                                                                                                                                                 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell signalling disorder; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiviral; antibacterial.
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0
                                                                                                                                                                                                                                                Length 1004;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human predicted caspase recruitment domain-14 (CARD-14).
                                                                                                                                                                                                                                                Score 930; DB 22;
Pred. No. 2.2e-91;
                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07165 standard; Protein; 1139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                 Claim 1; Fig 1A-1E; 109pp; English.
                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 700
                                                                                                                                                                                                                      1004 AA;
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                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07165:
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                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                         988
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                                                                                                                                                                                                                                                                                  (CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is used for the detection of modulators that modulates the ability of CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of nuclear factor-kappa B (NF-KB). The CARD-14 is useful for regulating growth and cell death and useful for the treatment of activation of sourcer. It is also useful for the treatment of autoimmune disorders (e.g., systemic lupus erythematosus), neurological disorders e.g., Alzheimer's and Parkinson's disease, inflammatory disorders, haematological disorders strokes, immune disorders (e.g., and propagatory disorders), myocardial infarctions, strokes, immune disorders and certain viral and bacterial infections.
                                                                                       An isolated caspase recruitment domain polypeptide useful for regulating growth and cell death and useful for the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is predicted human caspase recruitment domain-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response.
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/note= "cAMP- and cGMP-dependent protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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/note= "Protein Kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human caspase recruitment domain, CARD-11 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 884; DB 22;
Pred. No. 2.4e-86;
0; Mismatches 0;
                                                                                                                                                                                                      Disclosure; Fig 2A-2C; 109pp; English.
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100.08; F1
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Matches 171; Conservative
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2001-497073/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1139 AA;
                                 N-PSDB; AAD13448
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.850
.e= "Casein kinase II phosphorylation site"
                                        782
.e= "Casein kinase II phosphorylation site"
                                                                  "Protein kinase C phosphorylation site"
/note= "Casein kinase II phosphorylation site
                                                                        .828
e= "N-myristoylation site"
                                                                                                                                     "N-myristoylation site"
                                 "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 14A-14C; 145pp; English.
                "SH3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0507533.
; 2000US-0513904.
; 2000US-0685791.
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                                          /note= "Ca
382..1147
               /note= "Si
776..779
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853..858
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18-FEB-2000;
25-FEB-2000;
10-OCT-2000;
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        Domain
/note="cAMP- and cGMP-dependent protein kinase
phosphorylation site"
459..461
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "cAMP- and cGMP-dependent protein kinase
  phosphorylation site"
                                                                                                                                                                                                                                                                                                                                     /note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
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/note= "N-myristoylation site" 764..767
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578..581
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/note= "Casein kinase II phosphorylation site"
698..703
                                                                         ...292
ce- "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                  'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                       476..479
/note= "Casein kinase II phosphorylation site"
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'note= "Protein kinase C phosphorylation site"
                        ..165
:e= "Casein kinase II phosphorylation site"
                                         ..171
te= "Casein kinase II phosphorylation site"
                                                                                                                            . 245
te= "Protein kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
                                                                                           .195
.e= "Tyrosine kinase phosphorylation site"
                                                                   "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..641
te= "Glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                    'note= "Casein kinase II phosphorylation
108..510
'note= "Protein kinase C phosphorylation
                                                                                                                                                                                                         "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
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'10..715
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                                                                                                                                                                                                                                                                                   "N-glycosylation site"
                                                                                                                     "N-glycosylation site'
phosphorylation site"
                 "Coiled coil domain"
                                                                                                                                           ...285
+e= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "MAGUK domain"
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                                                                                                                                                                                                               .432
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                                                                                                             ..244
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                                                                                                                                                                                                                                                                                                                                                                                                                       .637
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                                                                                                                                                                                                                                                                                                                                                     558..560
         .431
                                                                                                                                                                                                                                                                                                                                                                                                               /note=
634..63
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129..43
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Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays The present sequence represents novel human caspase recruitment domain, CARD-11. The polynucleotide encoding this sequence was isolated from a human T-cell cDNA library. Also described are novel human sequences for CARD-9 and CARD-10 (AAU01205, AAU01206) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for /note= "N-myristoylation site" 1088..1091 /note= "Casein kinase II phosphorylation site" 1120..1123 /note= "Casein kinase II phosphorylation site" 875 ce= "Casein kinase II phosphorylation site" site" 926..929 /note= "Casein kinase II phosphorylation site" 935..937 .859 ce= "Protein kinase C phosphorylation site" 050..1018 note= "Tyrosine kinase phosphorylation site" 050..1055 'note= "Protein kinase C phosphorylation
.003..1006 "Casein kinase II phosphorylation "Guanylate kinase (GUK) domain" .922 .e= "N-myristoylation site"

(HYSE-) HYSEQ INC.

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treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11.

They can be used for the treatment of hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzhelmer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD composing the polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for regulating conducted in cancer. NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehaer's; Parkinson's disease; Hautington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                       RPRPVLLVPRAVGKILSEKLCLLQG - - - FKKCLAEYLSQEEYEAWSQRGDII - - QEGEVS
                                                                                                                                                                                                                                                                                                                     Length 1147;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                   26.1%; Score 242.5; DB 31.5%; Pred. No. 5.8e-17
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.5%; Pred. No. 5.8e-
Matches 57; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM38934 standard; Protein; 350 AA
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2000US-0598042.
2000US-0653450.
2000US-0663191.
2000US-0693036.
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                                                                                                                                                                                                                                                                                   1147 AA;
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19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                               Wang
                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%; Score 175.5; DB 22; Length 350; 32.8%; Pred. No. 2.1e-10; ive 24; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA synthesis; oligo-capping,
                               Qian XB,
Yang Y,
                            Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                        Example 3; SEQ ID NO 2079; 10078pp; English.
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                            Asundi V, Che
Wehrman T, Xu
Goodrich R,
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2000JP-0183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
                                                                                            WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 AA;
                                                            Zhou P,
                              Liu C,
Wang Z,
                                                                                                             N-PSDB; AAI58090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification.
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11-JAN-2000;
02-MAY-2000;
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                                                            Zhao QA,
                            Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AAM93822
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(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                     Bonne S,
                                                                      WPI; 2002-062246/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 58; Conserv
                                                                                                                    New polypeptide,
disease such as C
                                                                                        N-PSDB; AAS98203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been lesolated and nuclocities sequences of 5'— and 3'—ends of the cDNA molecules have been determined. For inners for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; plakoglobin; cytostatic; osteopathic; dermatological; cardiant; plakoglobin related disease; skin carcinoma; acantholytic disease; basal cell carcinoma; squamous cell carcinoma; Naxos disease; extramammary Paget's disease; hart disease; skin blistering; subcorneal acantholysis; Grover's disease; Hailey'Hailey's disease; Darier's disease; ctodermal dysplasia; skin fragility syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 SRI-RAIQESVGKK--HCLLELGARGVRELVQNEIYPIVIHVEVTEKNVREVRGLLGRPG
                                                     Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 746;
                                                                                                                                                                                                             Claim 8; SEQ ID NO 3879; 1380pp + sequence listing; English.
                                                     Hayashi K, Ishii S,
K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.9%; Score 175.5; DB 2
32.8%; Pred. No. 5.7e-10;
iive 24; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human plakoglobin interacting protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU73247 standard; Protein; 1032 AA
                                                       cawa T, Isogai T,
Sugiyama T, Nagai
                                                                                                                                                                              use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2000; 2000EP-0201668.
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                   (HELI-) HELIX RES INST
                                                       Nishikawa T,
                                                                                                        WPI; 2001-524255/58.
N-PSDB; AAK94778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Les 58, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       746 AA;
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                                                                         Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Matches
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The invention relates to an isolated plakoglobin interacting polypeptide (I). (I) is useful as a medicament and in the manufacture of a medicament for treating plakoglobin related diseases, such as skin carcinoma or an acantholytic disease, and to screen compounds that interfere with the interaction of the polypeptide with plakoglobin The plakoglobin related diseases include basal cell carcinoma, squamous cell carcinoma, extramammary Paget's disease. Naxos disease, heart diseases, skin blistering and acantholytic diseases such as subcorneal acantholysis, Grover's disease, Hailey-Hailey's disease or Darier's disease, and ectodermal dysplasia-yskin fragility syndrome. Auvi3245-AAVI7354 represent novel human plakoglobin interacting protein amino acid sequences and related sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | ||::| ||::| |||||906 SRI-RAIQESVGKK--HCLLELGARGVRELVQNBIYPIVIHVEVTEKNVREVRGLLGRPG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide, useful for treating skin carcinoma or acantholyti
disease such as Grover's and Darier's disease, comprises a protein
interacting with human plakoglobin and involved in transduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 1032;
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76..79 /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175.5; DB 2
Pred. No. 8.8e-10;
; Mismatches 88
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/note= "N-myristoylation
Vanlandschoot A;
                                                                                                                                                                                                                                                                                                               plakoglobin related signal to nucleus
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/note= "CARD domain"
68..70
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Figure 3; 98pp; English.
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"Casein kinase II phosphorylation site"

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18-FEB-2000;
25-FEB-2000;
                                    Modified-site
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                                                                                                                         Modified-site
                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                               10-OCT-2000;
                                                                                                                                                                                                                                                                                                             07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                            Bertin J;
                                                                                                           Domain
 //note= "N-myristcyration.513
//note= "Casein kinase II phosphorylation site"
                                                                                                                .295
.e= "Protein Kinase C phosphorylation site"
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ce= "Protein Kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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te= "Protein kinase C phosphorylation site"
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te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                               ..481
te- "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                  .573
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                        "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation site"
        phosphorylation site"
                             ..115
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                              "Tyrosine kinase phosphorylation site"
                                                                                                  .514
ce= "Protein kinase C phosphorylation
                                                                                                                               93..296
note= "Casein kinase II phosphorylation
09..314
                                                                                            "Leucine zipper homology region"
                                                                                                                                                                                                                                                                                                                                                                                                                              .641
ce= "Glycosaminoglycan attachment
                                                                                                                                                                                                                             "Leucine zipper homology
                                                                                                                                                                                                                                                                                            ..492
te= "N-myristoylation site"
                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                     "N-myristoylation site"
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/note= "SH3 domain"
712..715
/note= "N-glycosylation site"
714..717
                                                                                                                                                                                                                                                                         "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                          "N-glycosylation site"
                                                               "Coiled coil domain"
                                                                                                                                                                                       ...398
re= "Tropomyosin domain"
       "Protein kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΙΙ
                     'note= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
..693
re= "Casein kinase
                                                                                                                                                                                                                                                           "MAGUK domain"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N
303..605
                                                         .457
                                                                        . 207
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The present sequence represents novel human caspase recruitment domain, CARD-10. The polynucleotide encoding this sequence was isolated from a human skin cDNA library. Also described are novel human sequences for CARD-9 and CARD-11 (AAU01205, AAU01207) and rat CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the invention can be used for treating a disorder associated with abnormal levels of apoptosis by modulating the expression or activity of CARD-9, CARD-10, or CARD-11. They can be used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site"
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te= "Protein kinase C phosphorylation site"
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1021. 1026
/note= "N-myristoylation site"
/note= "Protein kinase C phosphorylation site"
1028. 1031
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                                                                                                                                                                                                                                                                                                                                          ..832
te= "Protein kinase C phosphorylation site"
                                      .751
-- "Casein Kinase II phosphorylation site"
                                                                                 .756
.e= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                           ...784
te= "Protein kinase C phosphorylation site"
                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                .870
.e= "Protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                           ...872
te- "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .885
te= "Casein kinase II phosphorylation
                    "Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                                               .1032
e= "Guanylate kinase (GUK) domain"
                                                                                                                                                                  .766
e= "N-myristoylation site"
                                                                                                                                                                                                                                                                               "N-myristoylation site"
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..918
re= "Amidation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
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N-PSDB; AAS05388.
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hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus), neurological disorders (e.g. Alzheimmer's disease), inflammatory disorders (e.g. Crohn's disease), and viral infection (e.g. HTV). The CARD polypeptide, polypucleotide and an antibody which selectively binds to CARD can be used in screening
                                                                             and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD sequences are potential targets for requiating inflammation, cancer, NF-kappaB signalling, stress-related response and apoptosis in human disease. A host cell containing a polynucleotide encoding CARD can be used to
                                                                                                                                                                                                                                                                                                                                                        846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                           CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                            SRI-RAIQESVGKK--HCLLELGARGVRERVONEIXPIVIHVEVTEKNVREVRGLLGRPG 962
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family protein - used for, e.g. investigation of tumour suppression and for development of anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                             3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR
                                                                                                                                                                                                                                                             Length 1032;
                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-dlg; dlg family; detection; carcinostatic mechanism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour suppressor; embryogenesis; regulation.
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                           18.2%; Score 169.5; DB 232.2%; Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by WAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW72748 standard; Protein; 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= unknown
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                                                                                                                                                                                                 create transgenic animals
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-568727/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human P-dlg protein
                                                                                                                                                                                                                             1032 AA;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                           57;
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                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   These proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the mouse guanylate kinase. The ger was isolated from a lambda-gt10 cDNA library of mouse 702/3 B lymphoma cells, using the corresp, human gene (AAT/17148) as a probe. The isolated gene fragment (800 bp) was cloned into pUC118. These proteins
          The present sequence is a human protein belonging to the dlg family (P-dig). P-dig is recognised by an antibody binding to the epitope: RECREPIXERDKYTORHSKE. The dlg family of proteins is involved in regulation of embryogenesis and in tumour suppression. P-dlg, and its associated polynucleotides and antibodies are useful in investigating mechanisms of tumour suppression and in the design and screening of potential anticancer agents.
                                                                                                                                                                                                                                                   495 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF----VDYKRR 549
                                                                                                                                                                                                                                                                                   SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                    NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding Herpes virus thymidine kinase enzyme - useful for inhibiting a pathogenic agent, a tumour cell or an auto:reactive immune cell
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                         ----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                        57;
                                                                                                                                                            Length 674;
                                                                                                                                                                                           Indels
                                                                                                                                                             DB 19;
                                                                                                                                                                                        64;
                                                                                                                                                            Score 128.5; DB Pred. No. 6e-05; ); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                             13.8%; Scc
26.7%; Pre
Live 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR93137 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse guanylate kinase protein.
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                           Best Local Similarity
Matches 55; Conserv
                                                                                                                                674 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93137;
                                                                                                                                   Sequence
                                                                                                                                                               Query Match
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     for ease
were fused to a hexa-His/thrombin cleavage site peptide sequence for ease of purification. The human and mouse guanylate kinase genes can be used to construct dual expression vectors confy. the human or mouse sequences and novel Herpes simplex virus (HSV) type-1 thymidine kinase mutants (AATO5187-91) which contain mutations in the region encoding residues 165-175. Vectors confy. the mutant and normal kinase sequences can be used to inhibit a pathogenic agent in a warm blooded animal e.g. viruses, bacteria or parasites, or a tumour cell or autoreactive immune
                                                                                                                                                                                                                                                                                                                                                    102 VNEKMAKKLKKGLQRLGTSEEQLLE---AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                              42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                         DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQGVRSIKKTDLCP--IYIF 121
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                        2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-------YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA sequence (III) of a polypeptide having human haematopoietic cell growth potentiating factor (HCGPF) activity.
                                                                                                                                                                                               27;
                                                                                                                                                                   Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth potentiating factor - prepd. from human peripheral blood derived
                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoimmune disease therapy; immunodeficient disease;
                                                                                                                                                                                               82:
                                                                                                                                                                  13.4%; Score 124.5; DB 1
25.5%; Pred. No. 3.2e-05;
ive 37; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinsuke T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP70243 standard; protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 62; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Junji H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86JP-0002633.
87JP-0002521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human haematopoietic cell
from gene obtd. using RNA
mononuclear cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          159 CVRQAIADEQKKVVWT 174
                                                                                                                                                                                             50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            marrow transplant
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                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                        198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nobukazu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP232707-A.
                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the mouse guanylate kinase (GK) protein. The invention relates to the generation of novel H8V-1 thymadine kinase (TK) or GK genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting abthogenic agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as AIDS, hepatitis,
The HCGPF exhibits immune control and haematopietic control functions over a wide range and may be used in the fields of immunodeficient diseases, autoimmune diseases, infectious diseases, hepatitis, nephritis, cancers and bone marrow transplantation.
                                                                                                                                                                                                                                                                                                                                                    42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                           Gaps
                                                                                                                                                                                                                            63
                                                                                                                                                                                             -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                               VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS
                                                                                                                                                                                                                          4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR
                                                                                                                                                                                                                                                                                              DIAAGDFIEQAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--IYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Herpesviridae thymidine kinase mutants - useful for treating
prostate hypertrophy, allergies, cystic fibrosis and Alzheimer's
                                                                                                                                                           27;
                                                                                                                       DB 8; Length 197;
                                                                                                                     13.1%; Score 121.5; DB 8; 25.5%; Pred. No. 6.7e-05; tive 39; Mismatches 77;
                                                                                                                                                                                         2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 25; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY07443 standard; Protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse guanylate kinase protein.
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   159 CVRQAIADEQKK 170
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180 ELKEALSEEIKK 191
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                                                                                                                                     Local Similarity
nes 49; Conserv
                                                                                    197 AA;
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                                                                                      Sequence
                                                                                                                       Query Match
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Length 198;

DB 20;

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(AJIN ) AJINOMOTO KK.
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                                         Similarity
198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                           Query Match
Best Local Simi
Matches 53;
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Sequence
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the mouse guanylate kinase (GK) protein. The invention relates to the generation of movel HSV-1 thymidine kinase (TK) or GK genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkratosis, psoriasis, prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as AIDS, hepatitis, intracellular parasitic diseases or bacterial infection.
                                                                                                                                                                                                                                                       102 VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                                                                                                                           42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                       Gaps
                                                                                                                  ---YLSQEEYEA 41
                                                                                                                                               4 PRPVVLSGPSGAGKSTLLKKLFQEHSSIFGFSVSHTTRNPRPGEEDGKDYYFVTREMMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   develop products for treating e.g. tumours, autoimmune diseases, allergies, restenosis or viral, bacterial or parasitic diseases
                                                                                     29;
                                                        Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Herpesviridiae thymidine kinase mutant nucleic acids
                                                                                       Indels
intracellular parasitic diseases or bacterial infection
                                                          DB 20;
                                                        13.1%; Score 121.5; DB 2 26.9%; Pred. No. 6.8e-05;
                                                                                                                  2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
                                                                                     37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               AA
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                                                                                                                                                                                                                                                                                                                                                                                              AAW97135 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse guanylate kinase protein.
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94US-0237592
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179 ATLKQALSEEIKKAQGT 195
                                                                                                                                                                                                                                                                                            SCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                       Conservative
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                                                                       Local Similarity
                             198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX15377
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                                                                                       53;
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97135;
                              Sequence
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wus sp
                                                                                                                                                                                                                                                                                            158
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                       Human haematopoietic cell growth potentiating factor; immune control; haematopoietic control functions; immunodeficient diseases;
                                                                                                                      42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                  VNEKMAKKLKKGLQRLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                                        4 PRPVVLSGPSGAGKSTLLKKLFQEHSSIFGFSVSHTTRNPRPGEEDGKDYYFVTREMMQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19..197
/note="A polypeptide with this sequence and a gene encoding it are claimed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of a polypeptide having human haematopoietic cell growth potentiating factor (HCGPF) activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant human haematopoietic cell growth potentiating factor used for immuno:deficient, auto:immune or infectious diseases, hepatitis, nephritis, cancer or bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kashima
                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13, claim 34; Fig 2 and Fig 5 and Fig 8; 58pp; English.
                               Indels
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Score 121.5; DB 20;
Pred. No. 6.8e-05;
7; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                             PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases; infectious diseases.
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                                                                                                                                                                                                                                                                                                                                                  A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="As above"
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                             37;
 13.1%;
26.9%;
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                                                                                                                                                                                                                                              SCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                    179 ATLKQALSEEIKKAQGT 195
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                               Conservative
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Homo sapiens
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                                   Seguence
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                                                          Query Match
                                                                             Matches
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SXSS
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                                                       7;
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The human gene was used to isolate the gene encoding the mouse guanylate kinase gene (AAT17149). These proteins were fused to as the hear-His/thrombin cleavage site peptide sequence for ease of purification. The human and mouse guanylate kinase gene can be used to construct dual expression vectors contg. the human or mouse sequences and novel Herspes simplex virus (HSV) type-1 thymidine kinase mutants (AAT05187-91) which contain mutations in the region encoding residues 165-175. Vectors contg. the mutant and normal kinase sequences can be
                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus; thymidine kinase; mutant; random library; vector; nuclectide binding site; inhibition; pathogenic agent; virus; bacterium; warm blooded animal; parasite; tumour cell; autoreactive immune cell; primer; PCR; amplification; mouse; human; guanylate kinase.
                                                                                                                                                                                  64 DIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATDLRP--1Y1S 121
                                                                                                                                                                       VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                       Gaps
                                                                                                                          42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHVS 101
                                                                              -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding Herpes virus thymidine kinase enzyme
                                                                                               4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - useful for inhibiting a pathogenic agent, a tumour cell or an auto:reactive immune cell
                                                      27;
                              Length 197;
                                                       Indels
                                                       78;
                                DB 9;
                               12.8%; Score 119.5; DB 9 25.5%; Pred. No. 0.00011;
                                                                            2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE--
                                                      38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 87-88; 124pp; English.
                                                                                                                                                                                                                                                                                                     AAR93136 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                         Human guanylate kinase protein.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                      49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                    CVRQAIADEQKK 170
                                                                                                                                                                                                                                         180 ELKEALSEEIKK 191
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                                            Similarity
         197 AA;
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         Sequence
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                                Query Match
                                              Local
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                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining activators or inhibitors of 'deregulated in hyperactive macrophage' (DHAM)-kinase for treating chronic inflammatory airway diseases, by measuring DHAM-kinase function after it is contacted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                               WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                              -----YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                   4 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 63
used to inhibit a pathogenic agent in a warm blooded animal e.g. vi
bacteria or parasites, or a tumour cell or autoreactive immune cell
                                                                                                                                                                                                     27;
                                                                                                                                            Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, DHAM-kinase inhibitor; guanylate kinase 1; PRK2; deregulated in hyperactive macrophage kinase inhibitor; GUK1; serin-threonin-kinase; PAK2; inflammatory condition; chronic inflammatory airway disease; chronic bronchitis; chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                     Indels
                                                                                                           Score 119.5; DB 10,
                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                              2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE-
                                                                                                                                                                       ; Pred. No. 0.00
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOEH ) BOEHRINGER INGELHEIM PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 47-48; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA015490 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human guanylate kinase 1 (GUK1).
                                                                                                                                            12.8%;
25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-2001; 2001WO-EP14844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2000; 2000US-257854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                       Local Similaire, nes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 CVRQAIADEOKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ELKEALSEEIKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mueller S,
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                                                                                                                                                                    Similarity
                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAL44148.
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                                                                                      197
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disease - {\tt COPD}). The present amino acid sequence represents the human guanylate kinase 1 ({\tt GUK1}).
                                                                                                                                                                          42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                           Query Match 12.8%; Score 119.5; DB 23; Length 197; Best Local Similarity 25.5%; Pred. No. 0.00011; Matches 49; Conservative 38; Mismatches 78; Indels 27; Gaps
                                                                                                                      159 CVRQAIADEQKK 170
                                         Sequence 197 AA;
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Search completed: January 22, 2003, 08:52:22 Job time : 35.8857 secs

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42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
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US-08-432-871C-51
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                                                                                                                                                                                                                                                                                                                                                        (without alignments) 429.229 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                    January 22, 2003, 08:52:30 ; Search time 12.2702 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RPRPVLLVPRAVGKILSEKL......VRQAIADEQKKVVWTEQSPR 179
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5: /cgn2_6/ptcdata/1/laa/FCTUS_COMB.pep:*
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                                     GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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US-09-150-460B-6
US-09-562-737-29
US-09-562-737-29
US-09-562-737-24
US-08-353-700-1
US-08-353-700-1
US-08-9562-737-24
US-08-353-700-1
US-08-150-460B-10
US-08-160-16-10
US-08-16-10-10
US-08-16-10-10
US-08-16-10-10
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: MCMASters, David D.
REFERENCE/DOCKET NUMBER: 34,963
REFERENCE/DOCKET NUMBER: 34,0052,409C1
TELLECOMMUNICATION INFORMATION:
                                         US-09-562-737-23
US-09-562-737-28
US-08-680-326-40
US-08-361-611-2
US-08-946-967-2
US-08-946-967-2
US-09-517-083-22
US-09-517-32-82
US-09-134-001C-5492
US-09-085-199B-2
US-09-085-199B-4
US-09-088-199B-4
US-09-088-189B-4
US-09-088-489-23
US-09-088-489-24
US-09-088-489-24
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APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
WIMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 121.5; DB 26.9%; Pred. No. 1e-05; tive 37; Mismatches
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STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/08432871C; Patent No. 5877010; GENERAL INFORMATION:
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TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 51:
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Matches 53; Conservative
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LENGTH:
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                                                                                    42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
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64 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQAVRSIKKTDLCP--IYIF 121
                                                          102 VNEKMAKKLKKGLORLGT-SEEQL---LEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                      Sequence 51, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCY/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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| TELEPAX: (206) 682-6031
| TELEX: 3723836
| INFORMATION FOR SEQ ID NO: 51:
| SEQUENCE CHARACTERISTICS:
| TENGTH: 198 amino acids
| TYPE: amino acid
| TYPE: amino acid
| TYPE: AMINO ACID | TYPE: DIOLOGY: 1inear
| MOLECTLE TYPE: protein
| US-09-270-956-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 ATLKQALSEIKKAQGT 195
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Best Local Similarity 26.98
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                       US-09-270-956-51
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, DAY46 D.
REFERENCE/DOCKET NUMBER: 24,0052.409C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%; Score 118.5; DB 2;
llarity 25.5%; Pred. No. 2.2e-05;
Conservative 38; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A. APPLICANT: Black, Margaret E. TITLE OF INVENTION: THYMIDINE KINASE MUTANTS NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                             APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
CORRESPONDENCE: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PRPVLLV-PRAVGKILSEKLCL----LQGFKKCLAE---
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      Sequence 49, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 372836
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 197 amino acids amino acid
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STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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180 ELKEALSEEIKK 191
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Best Local Similarity
Matches 49; Conserv
US-08-432-871C-49
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US-09-270-956-49
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SEQ ID NO 7
LENGIH: 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PRPVVLSGPSGAGKSTLLKRLLQAHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMOR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lee, Cheng-Chi
APPLICANT: Albrecht, Urs
APPLICANT: Eichele, Gregor
APPLICANT: Eichele, Gregor
APPLICANT: Eichele, Gregor
TITLE OF INVENTION: Mammalian Circadian Rhythym-Like Gene
TITLE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
PRIOR PLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,956

FILING DATE: 17-MAR-1999

CLASSIETCATION: 435

ATTORNEY/AGNT INFORMATION:

NAME: MCMASTERS 13,963

REFERENCE/DOCKET NUMBER: 24,0052.409C3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (206) 622-4900

TELEPAX: (206) 622-6031

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHRARATISTICS:

LENGTH: 197 amino acids

TYPE: ADDITION ACIDS
                6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 118.5; DB 4;
; Pred. No. 2.2e-05;
38; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PRPVLLV-PRAVGKILSEKLCL----LQGFKKCLAE-----
                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09150460B Patent No. 6190882 GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-270-956-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|:::| | |
180 ELKEALSEEIKK 191
                                                       Washington
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Best Local Similarity
                                                                                          98104-7092
          STREET: boccorry: Seattle
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US-09-150-460B-8
                                                                          COUNTRY:
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LENGTH: 798
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                                                                                                                                                                                                                                                                              149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS-----LEEGEPCS----- 194
                                                                                                                                                                                                                                                                                                                                     66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS-----LEEGEPCS----- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                       7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
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; OTHER INFORMATION: Peptide sequence of largest deduced open reading; OTHER INFORMATION: frame from RIGUI 3.0 US-09-150-460B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Peptide sequence of largest deduced open reading COTHER INFORMATION: frame from RIGUI 6.6 US-09-150-460B-7
                                                                                                                Length 798;
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APPLICANT: Albrecht, Urs
APPLICANT: Eichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhythym-Like Gene
FILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                 51; Indels
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Patent No. 6190882
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
APPLICANT: Blocht, Urs
APPLICANT: Bloche, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhythym-Like Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
                                                                                                                DB 4;
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Best Local Similarity 25.8%; Pred. No. 0.63;
Matches 39; Conservative 24; Mismatches 51;
                                                                                                             Query Match 9.3%; Score 86.5; DB Best Local Similarity 25.8%; Pred. No. 0.55; Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09150460B Patent No. 6190882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
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APPLICANT: Lee, Ch
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US-09-150-460B-6
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USA
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US-08-328-254-6
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                                                                                                                                                                                                                                                                                             LENGTH: 724
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                                                                                                                                                                                             OTHER INFORMATION: Protein sequence corresponding to RIGUI 4.7; Gene Bank OTHER INFORMATION: Accession Number: AF022991
                                                                                                                                                                                                                                                                                                                                                                                                                                    66 VESLMEKNTHALLDVQ-LDSVCTLHRMDIFPI-----VIHVSVNEKMAKKLKKGLQR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 RPIIILGPTKDRANDDLLSE---FPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEK 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHV- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Gaps
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                                                                                                                                                                                                                                                                                                                                                       7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence US-09-562-737-21
                                                                                                                                                                                                                                                                         Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 9.0%; Score 84; DB 4; Length 724; Best Local Similarity 19.2%; Pred. No. 0.91; Matches 40; Conservative 37; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09562737
Fatent No. 642867
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEY--
                                                                                                                                                                                                                                                                         9.3%; Score 86.5; DB 4;
25.8%; Pred. No. 1.1;
tive 24; Mismatches 51;
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 6
LENGTH: 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 -GTRFSELL--APQDVG-----VFYGSTAP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 DLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     699 E---IYHKVKRVIEDLSGPYIWVPARER 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             Best Local Similarity 25.8%
Matches 39; Conservative
                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    US-09-150-460B-6
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585 SREKKEKDIQAHKFLEAGOYNSHLMGTSVQSVRENAEQGKHCILQVSANAVRRLRAAHLH 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645 PIAISIRPRSLENVTEINKRITEEVARKAFDRATWLEQEFTE--------CFYAI 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 SQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIF 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5710022el Nuclear Mitotic Phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence
; OTHER INFORMATION: Sequence
12.09-562-737-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTONEY/AGENT INFORMATION:
ANNUREY/AGENT INFORMATION:
                                                                          GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83; DB 4;
Pred. No. 1.2;
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8.9%; Score 83; DB 4
Best Local Similarity 18.7%; Pred. No. 1.2;
Matches 29; Conservative 32; Mismatches
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 57100228
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
US-00-562-737-29
; Sequence 29, Application US/09562737
: Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 PROLENVLEINKSITEEQARKATDRATKL---EQEVTEC-------FSAIVE- 693
                                                                                                                                                                                                                                                                                                                                             92 DIFPIVIHVSVNEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 RPIIILGPTADRANDDLLSD---FPDKFGSCVEHTTRPKREYFIDGRDYHFVGSREKMEK 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEYL------SQEEYEA 41
                                                                                                                                                                                                                                                                                                                   44 QRGDII----QEGEVSGGRCWVTRHAVESLMEKN-----THALLDVQLDSVCTLHRM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                              8.7%; Score 81; DB 1; Length 2482;
23.7%; Pred. No. 11;
tive 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.6%; Score 80; DB 4; Length 724; Best Local Similarity 18.5%; Pred. No. 2.5; Matches 39; Conservative 36; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Herz, Joachim
APPLICANT: Gothbrach, michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT FAPPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 24
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 963 ------LDCLRRQYLSENEQ--WQQK 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GWSDLDGLLSCVRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WDSFEEIYHKYKRVIEDLSGAYIWVPARER 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09562737 Patent No. 6428967
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6: SEQUIBEC CHARACTERISTICS:
LENGTH: 2482 amino acids
                                                                                                    rrPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                          Matches 36; Conservative
                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-562-737-24
                                                                                                                                                                                                                                  Query Match
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RESULT 12 US-08-353-700-1

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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Ratiner, Jerome B.
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1598 QTGDMSLLSNLEGVVSANQCSVDEVFCSSLQEENLTRKETPSAPAKGVEELESLCEVYRQ 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 DIFPIVIHVSVNEXMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 QRGDII----QEGEVSGGRCWVTRHAVESLMEKN------THALLDVQLDSVCTLHRM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                         APPLICANT: YEN, TIMOTHY J.

APPLICANT: RATTHER, JEROME B.

TITLE OF INVENTION: NUCLEIC ACID ENCODING A

TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,

TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.6%; Score 80; DB
Best Local Similarity 23.7%; Pred. No. 21;
Matches 36; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1691 ------LDCLRKQYLSENEQ--WQQK 1708
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Sequence 1, Application US/08353700 Patent No. 5599919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dor
                                                                                                                                                                                                                                                                                                CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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87 TLHRMDIFPIVIHVS---VNEKMAKKLKKGLQRLGTSEEQ--LLEAARQEEGDLDRAPCL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08602656

Patent No. 5679571

GENERAL INFORMATION:
FITLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the TITLE OF INVENTION: Production and Use
TITLE OF INVENTION: Production and Use

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

8.2%; Score 76.5; DB 1; Length 460;
Best Local Similarity 24.8%; Pred. No. 3.3;
Matches 32; Conservative 21; Mismatches 43; Indels 3
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MDDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
OPPRATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,656
FILING DATE: 16 FEB-1996
                     PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTILING DATE: 27-AUGUST-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 523224man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1041
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 838-9200
TELEFAX: (212) 838-3846
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, NO. 5679571man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: BOER 1041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: P 43 28 829.4 FILING DATE: 27-AUGUST-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/289,709
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12-AUGUST-1994
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-289-709-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 YSSLAPDGW 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-602-656-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: Burtscher, Helmut; Lang, Gunter; Popp, Friedrich
TITLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the
TITLE OF INVENTION: Production and Use
TITLE OF INVENTION: Production and Use
NUMBER OF SEQUENCES:
ACCORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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8.6%; Score 80; DB 5; Length 3248;
Best Local Similarity 23.7%; Pred. No. 21;
Matches 36; Conservative 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                    COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1691 ------LDCLRKQYLSENEQ--WQQK 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 LAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER:
CLASSIFICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08289709
Patent No. 5523224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: not relevant not relevant
                                                                   COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
          Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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PCT-US95-16216-1
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Sequence 200, App Sequence 152, App

sequence 409, App Sequence 10062, A Sequence 518, App11 Sequence 44, App Sequence 44, App Sequence 674, Ap Sequence 374, Ap Sequence 374, Ap Sequence 374, App Sequence 32, App1 Sequence 9, App1 Sequence 78, App1 Sequence 78, App1 Sequence 78, App1 Sequence 13262, A Sequence 13262, A Sequence 1335, App1 Sequence 1335, App1 Sequence 1335, App1 Sequence 1335, App1 Sequence 326, App1

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0 US-09-783-320-46

0 US-09-994-288-5

0 US-09-72-200

2 US-10-078-929-152

0 US-09-815-242-10062

0 US-09-815-242-10062

0 US-09-815-242-1062

0 US-09-815-242-10540

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US-09-925-301-1335
US-09-866-582-39
US-09-978-729A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 4.0
   Matches 179; Conservative
   576
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6746
10048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-767-215-2
   TYPE: PRT
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   q
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Sequence 5, Appli
                                                                                                                                                      (without alignments)
500.428 Million cell updates/sec
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                                                                                                                                   January 22, 2003, 08:49:35; Search time 7.21774 Seconds
                                                                                                                                                                                                                                               1 RPRPVLLVPRAVGKILSEKL......VRQAIADEQKKVVWTEQSPR 179
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-032-159A-8
US-10-032-905-12
US-10-039-905-12
US-09-919-497-98
US-09-919-497-59
US-09-895-913A-358
US-09-895-913A-358
US-09-783-320-28
US-09-783-320-34
US-09-783-320-42
US-09-783-320-44
US-09-783-320-44
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US-09-783-320-44
US-09-783-320-48
US-09-783-320-48
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                                                                                                                                                                                                                                                                                                                                       122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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930
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq
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Perfect score:
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Database

Searched:

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61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVROAIADEOKKVVWTEOSPR 179
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Sequence 2, Application US/09767215

Patent No. US20020081636A1

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REPERENCE: 07334-142001

CURRENT APPLICATION NUMBER: US/09/767,215

CURRENT FILING DATE: 2001-01-22

PRIOR PELLING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 930; DB 10; Length 100.0%; Pred. No. 7e-87; tive 0; Mismatches 0; Indels
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US-09-767-215-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 RPRPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10032159A

Fatent No. US20020164703A1

GENERAL INFORMATION:

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

APPLICANT: Reed, John C.

TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,

TITLE OF INVENTION: CARD-DOMAIN COLISC AND METHODS OF USE

FILE REFERENCE: P-LJ 5100

CURRENT APPLICATION NUMBER: US/10/032,159A

CURRENT FILING DATE: 2000-12-19

PRIOR PELICATION NUMBER: US 60/257,457
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                                                                                                                                                                                                                                                                                                                                                                               Indels
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                APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.1%; Score 242.5; DB 9; Best Local Similarity 31.5%; Pred. No. 1.7e-16; Matches 57; Conservative 41; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                          Query Match 95.1%; Score 884; DB 10; Best Local Similarity 100.0%; Pred. No. 4.2e-82; Matches 171; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-032-159A-8
                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-767-215-5
  GENERAL INFORMATION:
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LENGTH: 1138
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                    Sequence 12, Application US/10029905
Patent No. US20020160438A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying compounds which positively
TITLE OF INVENTION: influence inflammatory conditions
FILE REFERENCE: 1/1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 98, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT PAPLICATION NUMBER: US 60/221,735
PRIOR APPLICATION NUMBER: US 60/221,735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.8%; Score 119.5; DB 9; 25.5%; Pred. No. 5.6e-05; tive 38; Mismatches 78;
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                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/029,905
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/257,854
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
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Best Local Similarity 25.5%
Matches 49; Conservative
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Best Local Similarity 21.29
Matches 35; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 100
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180 ELKEALSEEIKK 191
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LENGTH: 1736
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US-09-919-497-98
1244 E 1244
                                                                                                  US-10-029-905-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
LENGTH: 197
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Sequence 59, Application US/09919497
Fatent No. US-0020106662a1
Sequence 59, Application US/09919497
Fatent No. US-0020106662a1
SERERAL INFORMATION:
APPLICANT: Mutter, George L.
FITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR APPLICATION NUMBER: US 60/221,735
SPRIOR SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 767
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Patent No. US2002017445341

GENERAL INFORMATION:
APPLICANT: UNIVERSITY
APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
TILE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
FILE REFERENCE: 1463-PCT-US-00
CURRENT APPLICATION NUMBER: US/09/807,721
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: PCT/US01/06274
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 669
                                                              ------CFSAIVEGDSFE 741
647 EKLAREEPDIYQIAKSEPRDAGTDQRSSG---YIRLHTIKQIIDQDKHALLDVTPNAVDR 703
                                         --AKKLKKGLORLGTSEEQLLEAARQE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                              132 EGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 19.29
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-807-721-2
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APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1e1 Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALGARAM, Amal APPLICANT: ALGARAM, Amal APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francis
APPLICANT: Ownen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in tTITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT PAPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR PILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastsEQ for Windows Version 4.0
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                                           Gaps
                                                                             1 RPRPVLLVPRAVGKILSEKL---CLLQGF--KKCLAEYLS-----QEEYEAWSQRGDII 49
                                                                                                                                                           -- EGEVSGGRCWV-----TRHAVESLMEKNTHALLDV- 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 --EQLLEAARQEEGDLDRAPCLYSSLAPD-----GWSDLDGLLSCVRQAIADEQKK 170
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Length 669;
                                           Indels
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  DB 9;
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                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
                                                                                                                                                                                                                                                                81 -- QLDSVCTLHRMDIF----PIVIHVSVNEKM 106
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8.6%; Score 80;
25.7%; Pred. No.
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Patent No. US20020160456A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
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Patent No. US20020038011A1
GENERAL INFORMATION:
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                    25.7%;
                                         Conservative
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Matches 39; Conservative
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                    Best_Local Similarity
Matches 39; Conserv
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APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: NO. US20020038011A1e1 Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEX-0137-USA
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGHH: 211
                                  APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encodi
FILE REPERENCE: LEX-0137-USA
CURRENT ELILOS DATE: 2001-02-15
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 195
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8.3%; Score 77; DB 1

Best Local Similarity 24.5%; Pred. No. 1.2;

Matches 25; Conservative 21; Mismatches
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21; Mismatches
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Best Local Similarity 24.5%; Pred. No.
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US-09-783-320-36
; Sequence 36, Application US/09783320
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; Sequence 42, Application US/09783320
; Patent No. US20020038011A1
; GENERAL INFORMATION:
      Turner, C. Alexander Jr
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US-09-783-320-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
US-09-783-320-34
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CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 155
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-783-320-34
Sequence 34, Application US/09783320
Patent No. US20020038011A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09783320 Patent No. US20020038011A1
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Matches 25; Conservative
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APPLICANT: Walke, D. Wade
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: homo sapiens
US-09-783-320-26
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US-09-783-320-28
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APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020038011A1el Human Kinases and Polynucleotides Encodi
FILE REFERENCE: LEx.013.7 USA
CURRENT APPLICATION NUMBER: US 60/783,320
CURRENT FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-2
NUMBER OF SEQ ID NOS: 50
NUMBER: FastSEQ for Windows Version 4.0
SEQ ID NO 32
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tive 21; Mismatches 46; Indels
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                                                                                                                                                                                                   Sequence 32, Application US/09783320 Patent No. US20020038011A1 GENERL INFORMATION:
APPLICANT: Walke, D. Wade APPLICANT: Hu, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 24.59
Matches 25; Conservative
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                                                                                                                                              US-09-783-320-32
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                                                                                                                                                                              APPLICANT: Nepomnichy, Boris
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
TILLOANT: Turner, C. Alexander Jr
TILLOANT: Zambrowicz, Brian
TILLOANT: Zambrowicz, Brian
TILLOANT: Jambrowicz, Jambrow
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1.6;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 240
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                                               GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
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APPLICANT: Walke, D. Wade
APPLICANT: Hu, Yi
US20020038011A1
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ORGANISM: homo sapiens
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                                                                                                                                              Hu, Yi
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US-09-783-320-44
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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 22, 2003, 08:49:35; Search time 13.7137 Seconds Run on:

(without alignments)
1254.807 Million cell updates/sec

US-09-767-215-2\_COPY\_826\_1004 930 1 RPRPVLLVPRAVGKILSEKL.....VRQAIADEQKKVVWTEQSPR 179

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 DB Minimum Maximum

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dep			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
! !	130.5	14.0	,	7	T00346	hypothetical prote
7	122.5	13.2		~	539447	⊆
m	119.5	12.8	197	~	568864	
4	115.5	12.4		Н	KIPGGU	
S	110.5	11.9		7	T13703	tamA protein - fru
9	103.5	11.1		~	A47747	uo
7	100.5	10.8		~	A46431	tight junction-ass
8	4		1034	7	T22166	hypothetical prote
6	89.5	9.6	775	~	146236	0
10	88		1163	7	JE0366	unction
11	86.5	9.3	1290	~	T00018	period protein hom
12	98	9.5	886	7	н69378	conserved hypothet
13	84.5	9.1	429	7	F82679	conserved hypothet
14	84	9.0	724	7	JH0800	postsynaptic densi
15	84		767	7	T09599	postsynaptic densi
16			646	~	T02643	hypothetical prote
17			911	7	156552	O
18	82	8.8	849		S64732	scaffold attachmen
19	82		1225	7	A49464	chromosome segreda
20	80.5	8.7	1047	7	G90684	ATP-dependent dsDN
21	80.5	٠.	1047	7	C85535	
22	80		414	~	C69530	3-ketoacyl-CoA thi
23	80		720	7	A45436	synapse-associated
24	79.5	8.5	920	7	C96831	hypothetical prote
25	19		1744	7	F86161	F1003.10 protein -
26	78.5	8.4	379	~	T10588	UDPqlucose 4-epime
27	78.5	8.4	1920	7	A53188	pericentrin - mous
28	78.5	8.4	1927	7	G64585	cag pathogenicity
29	78	8.4	467	7	A57627	p55 erythrocyte me

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D82101	TIUBLI	A59431	T02749	154378	T48362	I39845	A54907	G02165	н87687	G82920	T00467	B35878	T02560	AI1720	T30818
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814	852	1023	471	1116	170	239	258	585	1203	191	375	406	748	998	1013
	4.	8.4	8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.2
						77 8.3	77 8.3	77 8.3	77 8.3	76.5 8.2			76.5 8.2	76.5 8.2	76.5 8.2

## ALIGNMENTS

R. Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, DNA Res. 5, 31-39, 1998
A.Title: Prediction of the coding sequences of unidentified human genes. IX. The comp A.Faference number: 214086; MUID:98290545; PMID:9628881
A.Accession: T00346
A.Accession: T00346
A.Raciuus: prediminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-1281 <NAG>
A.Residues: 1-1281 <NAG>
A.C.Coss.references: EMBL:AB011155; NID:g3043689; PIDN:BAA25509.1; PID:g3043690
A.Experimental source: brain; clone HJ0729 C.Species: Homo sapiens (man) C.Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000 X,Note: KIAA0583 C;Superfamily: guanylate kinase homology F;1102-1270/Domain: guanylate kinase homology <GKI> hypothetical protein KIAA0583 - human (fragment) C; Accession: T00346 ... 

10; Gaps 57; Query Match
14.0%; Score 130.5; DB 2; Length 1281;
Best Local Similarity 26.7%; Pred. No. 0.0018;
Matches 55; Conservative 31; Mismatches 63; Indels 57;

43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102 103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152 3 RPVL------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42 1157 qq qq οy ŏ

δŏ Q

LDGLLSCVRQAIADEQKKVVWTEQSP 178 153 1255 g ò

RESULT 2 S39447

guanylate kinase (EC 2.7.4.8) - bovine C;Species: Bos primigenius taurus (cattle) C;Daccies: 339447, 339448 C;Accession: 339447, 339448 R;Gaidarov, I.O.; Suslov, O.N.; Abdulaev, N.G. FEBS Lett. 335, 81-84, 1993 A;Title: Enzymes of the cyclic GMP metabolism in bovine retina. I. Cloning and expres A;Reference number: S39448; MUID:94063086; PMID:8243671

a

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A;Cross-references: EMBL:D83477; NID:g1498136; PIDN:BAA11923.1; PID:g1498137
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A;Molecule type: mRNA
A;Residues: 1-1367 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: tamou (tam)
A,Cross-references: FlyBase:FBgn0003177
                                                                                                                                                                                                                                    guanylate kinase (EC 2.7.4.8) - pig
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159 CVRQAIADEQKK 170
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                                            :::|::| 180 ELKEALSEEIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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Best Local Simi
Matches 50;
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A.Title: Human guanylate kinase (GUK1): CDNA sequence, expression and chromosomal localia A.Title: Human guanylate kinase (GUK1): CDNA sequence, expression and chromosomal localia A.Accession: 568864; MUID:96213684; PMID:8647247
A.Accession: 568864
A.Status: preliminary
A.Golcule type: mRNA
A.Residues: 1-197 < FIT>
A.Golcule type: MRNA
A
   A, Accession: $39447
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-198 (cAL)
A, Cross-references: EMBL:X67029; NID:9433073; PIDN:CAA47423.1; PID:9433074
A, Accession: $39448
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 10-17,24-32,35-82,90-97;121-126,139-146;149-154;178-182 (GA2)
C, Superfamily: quanylate kinase; quanylate kinase homology
C, Reywords: ATP; blocked amino end; magnesium; monomer; nucleotide binding; P-loop; phos F; 1897Domain: quanylate kinase homology (GKL)
F; 1187Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 VTREVMQRDIAAGDFIEHAEFSGNLYGTSKAAVRAVQAMNRICVLDVDLQGVRNIKKTDL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PRPVVLSGPSGAGKSTL-----LKKLLQEHGSIFGFSVSHTTRDPRPGEENGKDYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI
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C:Superfamily: quanylate Kinase; quanylate kinase homology
C:Keywords: nucleotide binding; P-loop; phosphotransferase
F:5-189/Domain: quanylate kinase homology <GKL>
F:11-18/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                ; Score 122.5; DB
; Pred. No. 0.001;
35; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           guanylate kinase (EC 2.7.4.8) 1 - human
                                                                                                                                                                                                                                                                                                                                                                                                       13.2%;
24.5%;
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S68864
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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tamA protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13.Aug-1999 #sequence_revision 13.Aug-1999 #text_change 17-Nov-2000
C;Accession: T13703
R;Takahisa, M; Togashi, S.; Suzuki, T.; Kobayashi, M.; Murayama, A.; Kondo, K.; Miya Genes Dev. 10, 1783-1795, 1996
A;Title: The Drosophila tamou gene, a component of the activating pathway of extramac A;Reference number: Z17700; MUID:96312452; PMID:8698238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-197 <282>
C;Superfamily: quanylate kinase; quanylate kinase homology
C;Keywords: acetylated amino end; ATP; magnesium; monomer; nucleotide binding; P-loop
F;4-188/Domain: guanylate kinase homology <GKI>
F;10-17/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-197 -2550-
R;Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
Eur. J. Blochem. 213, 263-269, 1993
A;Title: Purification and sequence determination of guanylate kinase from pig brain.
A;Reference number: $32545; MUID:93238695; PMID:8097461
A;Reference number: $32545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
Č; Spēcies: Sus scrofa domestica (domestic pig)
C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 197;
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                                                 C;Accession: S23776
C;Accession: S23776
C;Accession: S23776
C;Accession: S23776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
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146236

tight junction protein - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Species: 14-Feb-1997 #Sequence_revision 14-Feb-1997 #text_change 16-Dec-1998

C;Accession: 146236

R;Jesaitis, L.A.; Goodenough, D.A.

J. Cell Biol. 124, 949-961, 1994

A;Title: Molecular characterization and tissue distribution of 20-2, a tight junction
A;Molecule type: nucleic acid
A;Residues: 1-1745 <170>
A;Cross-references: GB:D14340; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371
A;Cross-references: GB:D14340; NID:g303709; PIDN:BAA03274.1; PID:d1003784; PID:g30371
A;Experimental source: F9 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:131200, NCBIP:131201)
C;Superfamily: guanylate kinase homology <GLGF domain homology
C;Superfamily: guanylate kinase homology <GLG3>
F;428-498/Domain: GLGF domain homology <GLG3>
F;645-794/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 46/2; 105/3; 187/3; 283/1; 365/3; 444/2; 501/2; 605/1; 688/1; 922/2;
                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F44D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS----CVRQAIADEQKKV 171
                                                                                                                                                                                                                                                                                                                                                                                       62 TRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKK-----GLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
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                                                                                                                                                                                                                                                                                                           Indels 27;
                                                                                                                                                                                                                                                         Length 1745;
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                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                        58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Coles, L. submitted to the EMBL Data Library, December 1995 A.Reference number: 219525 A.Accession: T22166 A.Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 25.6%; Pred. No. 2.4;
Matches 32; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                        35; Mismatches
                                                                                                                                                                                                                                                      Score 100.5;
                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                         10.8%;
24.1%;
                                                                                                                                                                                                                                                                                                           38; Conservative
                                                                                                                                                                                                                                                                                 Best Local Similarity
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A; Residues: 1-1034 <WIL>
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                                                                                                                                                                                                                                                         Query Match
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R.Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J.M.
R.Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J.M.
R.Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J.M.
R.Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.; Anderson, J.M.
A.Title: The tight junction protein 20-1 is homologus to the Drosophila discs-large tum
A.Reference number: A47747
A.Accession: A47747
A.Accession: A47747
A.Mosioules type: mRNA
A.Residues: 1-1736 AMILS
A.Gross-references: GB:L14837; NID:9292937; PIDN:AAA02891.1; PID:9292938
C.Superfamily: quanylate kinase homology; GLGF domain homology
C.Keywords: alternative splicing; membrane protein; phosphoprotein
F.181-248/Domain: GLGF domain homology GLG1>
F.181-248/Domain: GLGF domain homology GKG3>
F.416-486/Domain: GLGF domain homology GKG3>
F.533-782/Domain: guanylate kinase homology CKR1>
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tight junction-associated protein 20-1 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46431
R;Itoh, M.; Nagafuchi, A.; Yonemura, S.; Kitani-Yasuda, T.; Tsukita, S.; Tsu J. Cell Biol. 121, 491-502, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tight junction protein ZO-1 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
                                                                                                                                      647 EKLAREEPDIYQIAKSEPRDAGTDQRSSG---YIRLHTIKQIIDQDKHALLDVTPNAVDR 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AKKLKKGLQRLGTSEEQLLEAARQE 131
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                                                       Gaps
                                                                                                   3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
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                                                                                                                                                                                                       RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T
                                                                                                                                                                                                                                                                                                      SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK
     Length 1367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----INLNSMNDGW----YGALKEAVQQQQNQLVWVSE 790
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A; Reference number: A46431; WUID:93252986; PMID:8486731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
     DB 2;
                                                    64;
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  11.9%; Score 110.5; DE 23.4%; Pred. No. 0.12; iive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%; Score 103.5; DE larity 21.2%; Pred. No. 0.69; Conservative 36; Mismatches
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                                                    Conservative
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les 35; Conserv
                       Best_Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          170 KVVWTEQS 177
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A; Status: preliminary
       Query Match
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Matches
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Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus conserved hypothetical protein Aribaeoglobus fulgidus conserved further aribaeoglobus fulgid
Nature 389, 512-516, 1997
A;Title: Circadian oscillation of a mammalian homologue of the Drosophila period gene
A;Reference number: 214056; MUID:97472418; PMID:9333243
A;Accession: T00018
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                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1290 <TEL>
A;Cross-references: EMBL:AB002107; NID:q2506044; PIDN:BAA22633.1; PID:q2506045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 THALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEE- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 LPPERRGKGRSGTLATLQYALACVKQVQANQEYYQQWS-----LEEGEPCS----- 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LVPRAVGKILSEKLCLLQGFKKCLAE-YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHA 65
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milarity 26.1%; Pred. No. 12;
Conservative 33; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 86.5; D
Best Local Similarity 25.8%; Pred. No. 16;
Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 LGTSEEQLLEAARQEEGDLDRAPCLYSSLAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: brain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 17q12-13.1
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Best Local Similarity
Matches 43; Conservat
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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Accession: J5-30-1-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: J5036
R; Collins, J.R.; Rizzolo, L.J.
Biochem. Biophys. Res. Commun. 252, 617-622, 1998
A; Title: Protein-binding domains of the tight junction protein, ZO-2, are highly conservence number: JE0366, MuID: 99057550; PMID: 9837755
A; Reference number: JE0366
A; Astatus: preliminary
A; Residues: preliminary
A; Wolecule type: mRNA
A; Residues: 1-1163 <COL>
A; Cross-references: GB: AF085184; NID: 93820579; PIDN: AAC95469.1; PID: 93820580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               period protein homolog - human
C;Species: Homo Sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00018
R;Tei, H.; Okamura, H.; Shigeyoshi, Y.; Fukuhara, C.; Ozawa, R.; Hirose, M.; Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | ::|::|||||| :| ||||| 359 --VRLNTVRQIIEQDKHALLDVTPKAVDLLNYTQWFPIVIFFNPDSRQGVKTMR--QRLN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 PTSNKSSRKLYDQANKLKKT-CAHLFTATINLNSANDSW-----FGSLKDTIQHQQGEA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRL--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 -GTSEEQLLEAARQEEGDLDR--APCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             801 SNKSSRKLYEQANKLKKTCSHLFTATINLNSANDSW-----YGSLKDTIQQQQGEAVWV 854
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 775;
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             A;Reference number: A54475; MUID:94179414; PMID:8132716
A;Accession: 146236
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-775 <JES>
A;Crossreferences: GB:L27152; NID:9463047; PID:9507892
C;Genetics:
A;Gene: ZO-2
C;Superfamily: guanylate kinase homology; GLGF domain homology
F;101-1717/Domain: GLGF domain homology <GLGS
F;316-464/Domain: guanylate kinase homology <GKIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9;
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Best Local Similarity 22.7%; Pred. No. 4.9;
Matches 42; Conservative 30; Mismatches
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Matches 31; Conservative
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Search completed: January 22, 2003, 08:54:45
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C: Accession: F82679
Ranomyous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Ranomyous, The Xylella fastidiosa.
A: Anture 406, 131-157, 2000
A: Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A: Reference number: A82515; MUID: 20365717; PMID: 10910347
A: Note: for a complete list of authors see reference number A59328 below
A: Accession: F82679
A: Status: preliminary
A: Residuas: 14-29 < SINA
A: Residuas: 14-20 < SINA
A: Canargo, H. P.; Facincani, A. P.; Ferreira, A. J. S.
B: Ridmoson, A. J. G.; Relandor, F. C.; Arruda, P.; Franca, A. J. S.
B: Nocons, C.; Bloorna, C.; Bloorny, H.; Facincani, A. P.; Franca, A. J. S.
B: Nocons, M. L.; Remper, E. L.; Kitajima, J. P.; Krieger, J. E.; Kuramae, E. E.; Ligit Chado, M. A.; Madeira, A. M. B. Madeira, A. M. B.; Mack, C. P. M.; Miracca, E. C.; Miyaki, C. Y.; F. A.; Modo, M. A.; Madeira, A. M. B. M.; Madeira, M. C.; do Oliveira, M. S.; Santelli, R. V.; Sawasak
A: Authors: da Silva, A. C. R.; da Silva, F. R.; da Silva, A. M.; Silva, Jr., W. A.; da Silvai, A. Reference number: ASI328
A: Genetics: A. Genetics: A. C. R.; A. S. A. S. C. S. Santelli, R. V.; Sawasak
A: Genetics: A. Genetics: A. C. S. Santelli, R. V.; Sawasak
A: Genetics: A. Genetics: A. C. S. Saperianily: Haemophilus influenzae conserved hypothetical protein Hils90
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N.Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein PC; Species: Rattus norvegicus (Norway rat)

C; Species: Rattus norvegicus (Norway rat)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C; Accession: JH0800; S26407

R; Cho, K.O.; Hunt, C.A.; Kennedy, M.B.

Neuron 9, 929-942, 1992

A; Title: The rat brain postsynaptic density fraction contains a homolog of the drosophil A; Reference number: JH0800; MUID:93040233; PMID:1419001

A; Reference number: JH0800

A; Residues: 1-724 cCHO>

A; Residues: 1-724 c
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GLGF domain homology; guanylate kinase h
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C;Species: Homo sapiens (man)
C;Date: 16-Jul.1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C;Accession: T05599
R;Stathakls, D.G.; Hoover, K.H.; You, Z.; Bryant, P.J.
submitted to the EMBL Data Library, July 1998
A;Reference number: 216761
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                                42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHV- 100
                                                                                                                                           --SVNEKMA-KKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWS 151
                                                                                                                                                                                                                                                                         652 PRSLENVLEINKRITEEQARKAFDRATKLEQEFTE--------CFSAIVEGDSFE 698
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--LSQEEYEA 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-767 <STA>
A;Cross-references: EMBL:U83192; NID:g3318652; PID:g3318653
A;Experimental source: mammary
C;Genetics:
3 RPVLLV----PRAVGKILSEKLCLLQGFKKCL-----AEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: discs-large tumor suppressor; GLGF F; 208-28/Domain: GLGF Gomain homology <GLG>F; 478-755/Domain: S13 homology <SH3>F; 578-755/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : | : | | : | E---IYHKVKRVIEDLSGPYIWVPARER 766
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 22, 2003, 08:49:35 ; Search time 6.97715 Seconds (without alignments) 1064.082 Million cell updates/sec Run on:

US-09-767-215-2\_COPY\_826\_1004 930 1 RPRPVLLVPRAVGKILSEKL.....VRQAIADEQKKVVWTEQSPR 179 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9bx16 homo sapien	mus mus	Q9bx17 homo sapien	mus mus	homod	snw snw	pos	homo	s sns	Q07157 homo sapien	шns	mus m	Q92796 homo sapien	m snm		canis	homo s	canis		arch			homo	homo	Q62696 rattus norv	P32908 saccharomyc	Q8xxf9 ralstonia s	Q9qxy1 mus musculu	homo		mus m	4969	22
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ð	Query Match	100	9	9	σ	8	3	3	12.8	7	Н	0	0	ø.	7.6	9.7	9.6	9.5	9.5	9.3	9.5	9.0	9.0	9.0	8 6.8	8.0	8.8	8.8	8.7	9.8	8.5	8.4	8.4	8.4
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F_BACSU C_YEAST 3_HUMAN A_UREPA 1_MOUSE 2_CAREL 2_HUMAN 1_HUMAN D_MOUSE 5_HUMAN	1004 e upda ion upo 14 (Ci	Craniata; V Catarrhini;	on M. efano se re te ki ate N	Bonn part vatio	Bonn	enBan via B to e mic.	canc MAIN. DOMA TE KI SH3 . It . It oinfo ute. as lo
PYRF_BACSU KC2C_YEAST MMPB3_HUMAN KGUA_UREPA DNBI_SCWVC PERI_MOUSE AC12_CABEL INVO_AOTTR DLG2_HUMAN PNAD_MOUSE NATE_HUMAN PNAD_MOUSE NATE_HUMAN NATE_HUMAN	PRT; 10 ted) sequence up annotation i	Cran	78692; Jacobs Dist caspa Lanyla activ	56195; au O., Inding 3 acti	, O na	i.A.  the EMBL/GenB. NF-kappaB via nII. Bcll0 bind to Cytoplasmic Expressed in	in the other c NS 1 CARD DOMA NS 1 DZ/CHR D NS 1 GUANYLATE to contain a Si MART. is copyright. is copyright. ittute of Bioli atics Institut.
	D; Created) Last seg Last ann	lata,	1127 (',' J n S., ovel ed gu and and	Lchecong by	Micheau (2001).	N.A.  b) the B  c) the B  c) NF-kc  BC110  l BC110  N: Cyt  Expre	the 1 C2 1 C2 1 C2 1 C2 1 C2 1 C2
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	STAN (RE). 4 (RE). 4 (RE). 4 (RE). 4 (RE). 9	ARMA2. (Humar detazoa; utheria;	OM N.A. 92234; E Vang L., S.M., N CARD14 rane-ass ct with	M N.A. 55663; E artinon 2ARD-cor 10n and	Martinon F., 505:198-198	1-740 F  (x, and of the control of t	111s, but not in the other cancer ARITY: CONTAINS 1 DEZ/DHR DOMAIN. ARITY: CONTAINS 1 DEZ/DHR DOMAIN. ARITY: CONTAINS 1 GUANTLATE KINA. ON: Supposed to contain a SH3 doa TE, Pfam or SWART. S-PROT entry is copyright. It is the Swiss Institute of Bioinform ean Bioinformatics Institute. The
77 77 76 76 8 8 76 97 8 76 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	LT 1 CARE HUMAN STANDE Q9BXL6; Q9BVB5; 15-JUN-2002 (Rel. 41, 15-JUN-2002 (Rel. 41, 15-JUN-2002 (Rel. 41, 25-JUN-2002 (Rel. 41, 25-JU	CARD14 OR CARMA2. Homo sapiens (Human). Eukaryota; Metazoa; C Mammalia; Eutheria; P NCBI_TaxID=9606;	EQUENCE FRC EDLINE=2119 ENTIN J., W Trinivasula CARD11 and CARD1/membi hat interac Biol. Che	SEQUENCE FROM N.A. MEDLINE=21255663; PubMed=11356195; Gaide O., Martinon F., Mitheau O., Bonnet D., T "Carmal, a CARD-containing binding partner of B phosphorylation and NF-kappaB activation."; FEBS Lett. 496:121-127(2001).	ERRATUM. Gaide O., Ma FEBS Lett. 5	EQU ISS tra ubm !-	S3 cells, but not in the other cancer cell: SIMILARITY: CONTAINS 1 CARD DOMAIN: SIMILARITY: CONTAINS 1 DDZ/DHR DONAIN: SIMILARITY: CONTAINS 1 DDZ/DHR DONAIN: CAUTION: Supposed to contain a SH3 domain
	25.85		RRA		RR RP E	S E R R R R R R R R R R R R R R R R R R	

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SUBUNIT: CARD14 and Bc110 bind to each other by CARD-CARD
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noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 14 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                       DYEASEPLFKAVLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
                                                                                                                                                                                                                                                    GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
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                                                                                                                                                                                                                                                                                                                                                                 886 VTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFFIVIHVSVNEKMAKKLKKGLQRLGTS 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Binpl, a MAGUK family member linking protein kinase C activation Bcll0-mediated NF-kappa B induction."; J. Biol. Chem. 276:30589-30597(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
                                                                                                                                                                                                                                                                                                        Length 1004;
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                                                                                                                                                                                                                                                                                                         Score 930; DB 1; Length 1
Pred. No. 2.9e-73;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
                                                                                                                                                                                                                                                                                    7469B8B56BE06073 CRC64;
                                                                                                                                                                                             CARD. COIL (POTENTIAL).
                                                                                                                                   PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CAND; 1.
PROSITE; PS50052; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                             GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999 AA
 modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          AAH01326)
                                                      EMBL; AY022927; AAK64453.1; -.
EMBL; BC018142; AAH18142.1; -.
EMBL; BC001326, AAH01326.1; ALT_INIT.
InterPro; IPR000619; Guanjlate_kin.
InterPro; IPR001478; PD2.
SMART; SM00072; Gukc; 1.
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                                           EMBL; AF322642; AAG53403.1; -.
EMBL; AY032927; AAK54453.1; -.
                                                                                                                                                                                                                                                                                                         100.08;
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                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 179; Conservative
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 (Bimp2)

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 11 (CARD-containing MAGUK protein
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interaction (By similarity).
-!- SUBCELULAR LOCATION. Cytoplasmic (By similarity).
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.
-!- SIMILARITY: CONTAINS 1 DDZ/DHR DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- CAUTION: Supposed to contain a SH3 domain which is not detected PROSITE, Pfam or SWART.
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SEQUENCE FROM N.A.

BELLINE_21192234, PubMed=11278692;

Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,

Srinivasula S.M., Merriam S., Distefano P.S., Alnemri E.S.;

STARD11 and CARD14 are novel caspase recruitment domain

(CARD)/membrane-associated guanylate kinase (MAGUK) family members
that interact with Bollo and activate NF'kappab.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; BC004692; AAH04692.1; -.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50052; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS500106; PDZ; 1.
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15-JUN-2002 (Rel. 41, Last anno
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Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                         INTERFACTION.

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: Detected in adult peripheral blood leukocytes, trysues, spleen and liver. Also found in promyelocytic leukemia HL-60 cells, chronic myelogenous leukemia K562 cells, Burkitt's alymphoma Raji cells and colorectal adenocarcinoma SW480 cells. Not SIMILARITY: CONTAINS 1 CARD DOMAIN.

SIMILARITY: CONTAINS 1 CARD DOMAIN.

SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1026 AFEC-IAPANIEAVAAKNKHCLLEAGIGCTRDLIKSNIYPIVLFIRVCEKNIKRFRKLLP 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 RLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPRPVLLVPRAVGKILSEKLCLLQG---FKKCLAEYLSQEEYEAWSQRGDII--QEGEVS 55
                                                                                                               Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
Carmal, a CARD-containing binding partner of Bc110, induces Bc110
phosphorylation and NF-kappaB activation.";
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 242.5; DB 1; Length 1147; Pred. No. 2.1e-13; 41; Mismatches 76; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> L (IN REF. 2).
913A4B015D2B36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50209; CARD; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50052; GUANYLATE_KINASE_2; FALSE_NEG.
PROSITE; PS50106; PDZ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUANYLATE KINASE.
 Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:16393; CARDII.,
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PD2.
SMART; SM00228; PD2; 1.
                      SEQUENCE FROM N.A. MEDLINE-21255663; PubMed-11356195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF322641; AAG53402.1; -.
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123 442
673 748
966 1133
808 808
1147 AA; 132641 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.1%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 31.5
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil
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                                                                                                      ERRATUM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase recruitment domain protein 10 (Bcl10-interacting MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 IRGLIGRPGWRDSELLRQCRGSEQWLWGLPCSWVQVPAHAWGHAEELAKVVRGRILQEQA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interaction. They both participate in a complex with MALT1, where MALT1 binds to Bcl10.
--- TISSUE SPECIFICITY: Highly expressed in kidney, heart followed by brain, lung, liver, skeletal muscle and testis.
--- SIMILARITY: CONTAINS I CARD DOWAIN.
--- CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         834 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEEQCTSSAPGAPKAWPATAGL- 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 QEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GSR----IRAIQESVGKK--HCLLELGARGVRELVHSEVYPIVIHVEVTEKNVRE 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 LKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Binpl, a MAGUK family member linking protein kinase c activation to Bcll0-mediated NF-kappa B induction.",
J. Biol. chem. 276:30589-397(2001).
-: FUNCTION: Activates NF-kappaB via Bcll0 and IKK.
-: SUBUNIT: CARD10 and Bcll0 bind to each other by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEY------EAWSQRGDII 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lucas P.C., Ruland J., Benito A.,
                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%; Score 185.5; DB 1; Length 1021; 31.0%; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21391892; PubMed=11387339;
MCAllister-Lucas L.M., Inohara N., Lucas P.C., Ruland J., Ber
M.J. (J., Chen S., Chen F.F., Yamaoka S., Verma I.M., Mak T.W.,
Nunez G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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1021 AA; 114413 MW; 4811A09BDB8F792C CRC64;
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1021 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50209; CARD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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450
565
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RLVWVER 1008
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 KVVWTEQ 176
                                                                                                                                                                                                                                       CARDIO OR BIMPI
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RM MAIDINE-2005/155; Pubbed-10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,

RA BURDINE-2005/155; Pubbed-10591208;

RA BURDINE-2005/155; Pubbed-10591208;

RA BITG C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burd C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burd C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burd C.P., Blakey S.E., Bridgeman A.M., Buck D., Chen Y. Clark G.,

RA BITG C.P., Dockree C., Collier R.E., Connor R.,

RA Clegg S.M., Cobley V.E., Collier R.E., Connor R.,

RA Clegg S.M., Cobley V.E., Collier R.E., Connor R.,

RA BURD K.E., Rey J.M., Flenning K., Fernorb L., Garner A.A.,

Gibert J.G., Goverd M.E., Grafham D.V., Griffiths M.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Boxis A.M., Kinga A.,

Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

Marcha J.D., Mashreghi Wohammadi M., Matthews L.H., Mccann O.T.,

RA Dottin S. Shra H.K., Skuce C.D., Smalley S., Morthmore B.J.C.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

Willips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

Williams L., Milliams S.A., Williamson H., Willew J.D.,

RA Minoshima S., Kawasaxi K., Sasaxi T., Abakawa S., Rudoh J.,

RA Bhirtan A., Shibuya K., Sasaxi T., Abakawa S., Rudoh J.,

RA Dorman A., Fang F., Fu Y. Hu P., Hu P., Hua A., Kenton S., Lai H., Lao D. H.,

RA Dorman A., Fang F., Fu Y. Hu P., Hu P., Malaj E., Nguyen T., Pan H.,

RA Dorman A., Fang F., Fu Y. Hu P., Hua A., Kenton S., Raban H., Bonnan A., Fang F., Wh T., Whiteley D., Wollden M., Wallson D., Shall S., Maray J., Miller S., Matsay J., Miller S., Matsay J., Miller S., Martsy J., Miller S., Brider P., Walker C., Wang C., White J., Whitel S., Wollden M., Zhang G., Chasse S., Murray J., Miller S., Budarf M., Langell B.S., Slaikh T., Kurahashi H., Saltes P., Beller D., Saldir H., Saltes B., Bendel J. A., Haller R., Solden D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-21292987; PubMed-11259443;
Wang L., Guo Y., Huang W.-J., Ke X., Poyet J.-L., Manji G.A.,
Marriam S., Glucksmann M.A., DiStefano P.S., Alnemri E.S., Bertin J.;
"CARR10 is a novel caspase recruitment domain/membrane-associated
guanylate kinase family member that interacts with Bcl10 and activates
                                                                 09BWT7; 09UGRS; 09UGRG; 09Y3H0; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Caspase recruitment domain protein 10 (CARD-containing MAGUK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.; FEBS Lett. 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21255663; PubMed=11356195;
Gaide O., Martinon F., Micheau O., Bonnet D., Thome M., Tschopp J.;
"Carmal, a CARD-containing binding partner of Bcll0, induces Bcll0
phosphorylation and NF-KappaB activation.";
FEBS Lett, 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  PRT; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 276:21405-21409(2001)

    (Carma 3)
    CARD10 OR CARMA3.

                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF-kappa B."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           э;
                                                                                                                                                                                                                             interaction. They both participate in a complex with MALT1, where MALT1 binds to BOL10 (By similarity).
SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
TISSUE SPECIFICITY: Detected in adult heart, kidney and liver:
Inower levels in intestine, placenta, muscle and lung. Also found in fetal lung, liver and kidney.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 CWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       846 RPVVLLPECLAPRLIRNLLDLPSSRLDFQVCPAESLSGEELCPSSAPGAPKAQPATPGLG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRI-RAIQESVGKK--HCLLELGARGVRERVQNEIYPIVIHVEVTEKNVREVRGLLGRPG 962
                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: Supposed to contain a SH3, a PDZ and a guanylate kinase-like domain. But none of these 3 domains are detected by PROSITE, Pfam or SMART.
Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Redra D.
S., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RPVLLVPRAVGKILSEKLCLLQG----FKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 WRDSELLRQCRGSEQVLWGLPCSWVQVPAHEWGHAEELAKVVRGRILQEQARLVWVE 1019
Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra I
Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Ref.4 sequence differs from that shown due to various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.2%; Score 169.5; DB 1; Length 1032; 32.2%; Pred. No. 4.1e-07;
                                                                                                                                                                       -i- FUNCTION: Activates NF-kappaB via Bc110 and IKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 Q -> R (IN REF. 4).
17 K -> KQ (IN REF. 4).
17 R -> L (IN REF. 4).
115946 MW, 8377319A882A0949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate Kinase (EC 2.7.4.8) (GMP Kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 AA
                                                                                                              "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene identification problems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50209; CARD; 1.
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                                                                                                                                               Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
456
574
289
917
932
                                                                                         Tilahun Y., Wright H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
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Q64520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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DOMAIN
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KGUA_MOUSE
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MEDLINE=94271265; PubMed=7911663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGUA_HUMAN
Q16774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunt D.M.;
                                                                                                                                                                                                                                                                                                                                               INIT_MET
NP_BIND
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                             MEDLINE-96279248; PubMed-8663313;
Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
"Cloning, characterization, and modeling of mouse and human guanylate
kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 DIAAGDFIEHAEFSGNLYGTSKEAVRAVQAMNRICVLDVDLQGVRSIKKTDLCP--IYIF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 VNEKMAKKLKKGLQRLGTSEEQLLE···AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PRPVLLV-PRAVGK-ILSEKL----CLLQGFKKCLAE------YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                       J. BIOL. Chem. 271:16734-16740(1996).
-i- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP-
-i- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 197;
                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Kinase; ATP-binding; Acetylation.
INIT_MET 0 0 BY SIMILARITY.
NP_BIND 10 17 ATP (BY SIMILARITY).
MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 197 AA; 21787 WW; 332403BF0DICCFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                           -! - SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 124.5; DB 1
25.5%; Pred. No. 0.00051;
tive 37; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AA
                                                                                                                                                                                                                                                                                                                                                          PS00856; GUANYLATE_KINASE_1; 1. PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                               SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      MGD; MGI:95871; Gukl.
InterPro; IRR000619; Guanylate_kin.
Pfam; PfC00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                              EMBL; U53514; AAC52652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 CVRQAIADEQKKVVWT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 TLKQALSEEIKKAQGT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
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P46195;
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
PROSITE;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 RPIYIFVQPPSLDVLEQRLR---QRNTETEESLAKRLAAARADMESSKEPGLFDLIIVN- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 FPIVIHVSVN--EKMAKKLKKGLQRLGTSEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::| : | | | | : : | | : | | 5 VIREVMQRDIAAGDFIEHAEFSGNLYGTSKAAVRAVQAMNRICVLDVDLQGVRNIKKTDL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PRPVVLSGPSGAGKSTL-----LKKLLQEHGSIFGFSVSHTTRDPRPGEENGKDYYF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
Gaidarov I.O., Suslov O.N., Ovchinnikova T.V., Abdulaev N.G.;
"Guanylate kinase from bovine retina: isolation, primary structure,
and expression in E. coli.",
and expression. E. coli.",
-!- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
-!- CAPALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96213684; PubMed-8647247;
Fitzgibbon J., Katsanis N., Wells D., Delhanty J., Vallins W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human guanylate kinase (GUK1): cDNA sequence, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AA; 21778 MW; 5CB5DD007BC15C62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 122.5; DB 1
Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Kinase; ATP-binding; Acetylation. INIT_MET 0 0 BY SIMILARITY.
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01-NoV-1997 (Rel. 35, Last sequence update)
01-NOV-2002 (Rel. 41, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 WSDLDGLLSCVRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 -DSLDKAYWALKEALSEEIKKAQGTGQS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000619; Guanylate_kin.
Pfam; PF00625; Guanylate_kin; 1.
SMART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X67029; CAA47423.1; -. HSSP; P15454; 1GKY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
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NCBI_TaxID=9606;
                                   NCBI_TaxID=9823;
                                                                    rissue=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZO1_HUMAN
Q07157;
                                                                                                                                                                                                                                                         NP_BIND
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                         brain.";
                                                        SECUENCE
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ZO1_HUMAN
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          MEDLINE-96279248; PubMed-8663313;
Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
"Cloning, characterization, and modeling of mouse and human guanylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DIAAGDFIEHAEFSGNLYGTSKVAVQAWNRICVLDVDLQGVRNIKATDLRP--IYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 VNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDGWSDLDGLLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 WSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PRPVVLSGPSGAGKSTLLKRLLQEHSGIFGFSVSHTTRNPRPGEENGKDYYFVTREVMQR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PRPVLLV-PRAVGKILSEKLCLLQ-----GFKKCLAE------YLSQEEYEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                        DB 1; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                    0 0 BY SIMILARITY.

10 17 ATP (BY SIMILARITY).

10 17 ACEPYLATION (BY SIMILARITY).

196 AA: 21594 MW. C4727A7E2AA261B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 119.5; DB 1; 25.5%; Pred. No. 0.0014; Witnest 78;
                                                                                                                                                                                                                                                                                                                 KGUA_PIG STANDARD; PRT; 197 AA. p31006; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                   J. Biol. Chem. 271:16734-16740(1996)
                                                                                                                                                                                                                                                                 EMBL; BC006249; AAH06249.1; -. BEMBL; BC00934; AAH09914.1; -. HSSP; P15454; IGKY.
                                                                                                                                                                                                                                                         EMBL; L76200; AAC37598.1; -.
 Lett. 385:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                         Genew; HGNC:4693; GUK1.
MIM; 139270; -.
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179 ELKEALSEEIKK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 49; Conserv
                   SEQUENCE FROM N.A.
                                                                                       SEQUENCE FROM N.A.
                                                                                                  TISSUE-Lung
                                                          kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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  FEBS
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KGUA_PIG
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MEDLINE-93238695; PubMed=8097461; 2schocke P.D., Schiltz E., Schulz G.E.; "Purification and sequence determination of guanylate kinase from pig
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B.M.; Panning A.S., Jameson B., van Itallie C., Manderson J.M.; Panning A.S., population junction protein ZO-1 is homologous to the Drosophila discs-large tumor suppressor protein of septate junctions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
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01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona
occludens 1 protein) (Tight junction protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP--:- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
-:- SUBUNIT: MONOMER.

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ACETYLATION.
CF492B786FCC4E6E CRC64;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%; Score 115.5; DB 1; 24.0%; Pred. No. 0.0031; ative 35; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PRPVLLV-PRAVGKILSEKLCLLQGFKKCLAE------
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PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
Transferase; Kinase; ATP-binding; Acetylation.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1736 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. 213:263-269(1993).
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SMART; SM00072; GuKc; 1.
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                                                                                                                                                                                                      Homo sapiens (Human).
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132 EGDLDRAPCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                      ZO1_MOUSE
ID ZO1_M
                                        761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9:
                                                                                                                                                                                                                                                                                                                                               MICHT BE INVOLVED IN STABLLIZING JUNCTIONS. THE ALFHA DOMAIN MICHT BE INVOLVED IN STABLLIZING JUNCTIONS.
SUBCELLIANT LOCATION: PERIPHERAL MEMBRARE. CYTOPLASMIC SIDE.
MOVEMENT OF 20-1 FROM THE CYTOPLASM TO MEMBRANE IS AN EARLY EVENT OCCURRING CONCURRENTLY WITH CELL-CELL CONTACT.
SHORT FORM; ARE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCTS. THE SHPHA-CONTAINING ISOFORM IS FOUND IN MOST TESSUE SPECIFICITY: THE ALPHA-CONTAINING ISOFORM IS FOUND BOTH IN ENDOTHELIAL CELL JUNCTIONS. THE SHORT ISOFORM IS FOUND BOTH IN ENDOTHELIAL CELLS AND THE HIGHLY SPECIALIZED EPITHELIAL JUNCTIONS.
PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHRMDIFPIVIHVSVNEKM-------AKKLKKGLQRLGTSEEQLLEAARQE 131
Proc. Natl. Acad. Sci. U.S.A. 90:7834-7838(1993).
-!- FUNCTION: THE N-TERMINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL REQUIRED FOR TIGHT JUNCTION ASSEMBLY, WHILE THE C-TERMINAL MAY HAVE SPECIFIC PROPERTIES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 domain; Alternative splicing; Repeat; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 103.5; DB 1; Length 1; Pred. No. 0.41; 36; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508D01B7A0814FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0056; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3.
GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001619; Guanylate_kin.
InterPro: IPR001418; PDZ.
InterPro: IPR001452; SH3.
InterPro: IPR001452; SH3.
InterPro: IPR000906; ZUS.
Frām: PF00625; PDZ; 3.
Frām: PF00625; Guanylate_kin; 1.
Frām: PF00791; ZUS; 1.
SMART: SM00712; Gukc; 1.
SMART: SM00728; PDZ; 3.
SMART: SM00326; SH3; 1.
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PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L14837; AAA02891.1; -.
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21.2%;
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Best Local Similarity 21.2'
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A47747; A47747.
HSSP; P31016; 1BFE.
Genew; HGNC:11827; TJP1.
MIM; 601009; -
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1236
1420
989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tight junction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@liberine.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells is identical to 20-1, a tight junction-associated protein in epithelial cells: CDNA clouing and immunoelectron microscopy.";

J. Cell Biol. 121:491-502(1993).

J. Cell Biol. 121:491-502(1993).

HAVE SPECIFIC PROPERINAL MAY BE INVOLVED IN TRANSDUCING A SIGNAL REQUIRED FOR TIGHT JUNCTION STHE ALPHA DOMAIN MILE THE C-TERMINAL MAY BE INVOLVED IN STRAILIZING JUNCTIONS.

HAVE SPECIFIC PROPERINES OF TIGHT JUNCTIONS. THE ALPHA DOMAIN MICHT BE INVOLVED IN STRAILIZING JUNCTIONS.

C.: SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND 20-3.

MOVEMBRY OF 20-1 FROM THE CYTOPLASM TO MEMBRANE IS AN EARLY EVENT OCCURRING CONCURRENTLY WITH CELL-CELL CONTACT (BY SIMILARITY).

C.: SIMILARITY: CONTAINS 1 SH3 DOMAINS.

C.: SIMILARITY: CONTAINS 1 SH3 DOMAIN.

C.: SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                     Itoh M., Nagafuchi A., Yonemura S., Yasuda-Kitani T., Tsukita S., Tsukita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "The 220-kD protein colocalizing with cadherins in non-epithelial
                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein) (Tight junction protein 1).
...-INLNSMNDGW-----YGALKEAVQQQQNQLVWVSE 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Membrane.
PDZ 1.
PDZ 2.
                                                                                             PRT; 1745 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:98759; Tjpl.
InterPro; IPR000619; Gunnylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
InterPro; IPR000906; ZU5.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93252986; PubMed-8486731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00791; 2U5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D14340; BAA03274.1; -. PIR; A46431; A46431.
HSSP; P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tight junction; SH3 domain;
DOMAIN 23 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
SMART; SM00218; ZUS; 1.
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                             ZO1_MOUSE
P39447;
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SMART; SM00228; PDZ; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
                                                                                                                                                                     Gaps
                                                                                                                                                                                                      EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN tinnction protein ZO-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein 2).
                                                                                                                             Length 1745;
                                                                                                                                                                     Indels
                                                                                            C3DA2C0A9F411F66 CRC64;
                                                                                                                           ; Score 100.5; DB 1;
; Pred. No. 0.75;
35; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                     139 PCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                       772 TINLNSM-NDGW-----YGALKEAIQQQQNQLVWVSE 802
                 SH3.
GUANYLATE KINASE.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1167 AA
 PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1341872; Tjp2.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00625; Guanylate_kin; 1.; SM00072; GuKc; 1.
                                                                                            AA; 194710 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                 10.8%;
24.1%;
                                                                                                                         Query Match
Best Local Similarity 24.19
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00018; SH3; 1.
Pfam; PF00595; PDZ; 3.
 502
584
794
1247
1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P31016; 1BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
 421
516
644
1242
1424
1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZOZ_MOUSE
Q9Z0U1:
                                                                                            SEQUENCE
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                     DOMAIN
                                                         DOMAIN
                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                        32
                                                                                                                                                                                                                                           629
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ZO2_MOUSE
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"Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 6:337-345(1999).

-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR SUBUNIT NR2B (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 RPVVLFGPIADIAMERLANELPDLFQTAK-----TEPKDAGSEKSSGV----- 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CWYTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRL- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- VRLNIVRQIIEQDKHALLDVTPKAVDLLNYTQWFPIVIFFNPDSRQGVKIIR--QRLS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GTSEEQLLEAARQEEGDLDR--APCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| :| :| :| :| :| 812 PISNKSSRKLFDQANKLKKTCSHLFTATINVNSANDGW-----FGSLKDSIQQQQNEAV 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RPVLL----VPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makino K., Kuwahara H., Masuko N., Nishiyama Y., Morisaki T., Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.; Cloning and characterization of NE-dig: a novel human homolog of Drosophila discs large (dlg) tumor suppressor protein interacts with APC protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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                                                                                                                                                                                                                                                                                                                                                                             Length 1167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                             MW; F15DA3EBC3F9434F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein (Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
              PROSITE: PS00856: GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE: PS50052; GUANYLATE_KINASE_1; 1.
PROSITE: PS50052; GUANYLATE_KINASE_2; 1.
PROSITE: PS50002; SH3: 1.
Tight junction; SH3 domain; Repeat; Membrane.
DOMAIN 10 97 PDZ 1.
DOMAIN 287 365 PDZ 2.
DOMAIN 489 570 PDZ 3.
DOMAIN 678 858 GUANYLATE KINASE.
DOMAIN 1139 1142 POLY-GLU.
SEQUENCE 1167 AA; 131614 MW; F15DA3EBG3F9434F C
                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                          Pred No. 1.9;
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 AA
                                                                                                                                                                                                                                                                                                                                                                                      Score 93.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 330-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal brain;
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Local S...
43;
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Q92796; Q9U
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUANYLATE KINASE.

PRALADNISHNSSICZIGAVESKVSYPAPPOVPPTRYSPI
PRHMALBEDFT -> AARREGGAMERAKFSGSGLAMGLGS
ASASAWRRASORWAWPLRSLRPGGDA (IN REF. 2).
DFPGLSDDYCGANL -> SIKTKRKKSFRLSRKPFFYKSK
BMAQDESSIQDGCYTSNTSDSESSS (IN REF. 2).
3D7312EC4713F04E CRC64;
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 1 GUANYLATE KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 VSREQMEKDIQDNKFIEAGQFNDNLYGTSIQSVRAVAERGKHCILDVSGNAIKRLQQAQL 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 FPIVIHV---SVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    737 YPIAIFIKPKSIEALMEMNRQTYEQANKIYDKAMK-LEQEFGE-----YFTAIVQG- 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (Discs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 91; DB 1,
19.6%; Pred. No. 2.1;
ative 37; Mismatches
                                                                                                                                                                                                                                                 Pfan; PP00018; SH3; 1.
Pfan; PP0055; PD2; 3.
Pfan; PP0055; PD2; 3.
Probom; PD000066; SH3; 1.
SWART; SW00728; PD2; 3.
SWART; SW00288; PD2; 3.
PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         PDZ 1.
PDZ 2.
PDZ 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                             InterPro; IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 SDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              788 DSLEEIYNKIKQIIEDQSGHYIW 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817 AA; 90344 MW;
                                                                                                                                                           EMBL; AB033058; BAA86546.1;
HSSP; Q12959; 1PDR.
Genew; HGNC:2902; DLG3.
MIM; 300189; -
                                                                                                                                                   EMBL; U49089; AAB61453.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                           InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             SH3 domain; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large homolog 3).
DLG3 OR DLGH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLG3_MOUSE
P70175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Brain;
STRAIN=C57BL/6; TISSUE-Brain;
Schmutz N., Makino S., Yagi T.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
                                                                                                                                         -:- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-:- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-:- SIMILARITY: CONTAINS 1 GUANYLAFE KINASE-LIKE DOMAIN.
-:- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 FPIVIHVSVNEKMAKKLKKGLQRLGTSEEQLLEAARQEEGD-----LDRAPCL-----Y 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           769 YPIAIFIKPK------SIEALMEMNRRQTYEQANKIFDKAMKLEQEFGEY 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLG3_RAT STANDARD; PRT; 849 AA.
062936; P70547;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (PSD-95/SAP90 related protein 1) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF3EF2D7513538EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2.7; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   813 FTAIVOG-DSLEEIYNKIKQIIEDQSGHYIW 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00856; GUANYLATE_KINASE_1; 1. PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PD2; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 SSLAPDGWSDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.7%; Score 90;
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PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3
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Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849 AA;
                                                                                                                      SUBUNIT NR2B.
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SEQUENCE
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                                                                                                                                                                                                                                                                                         Irie M., Hata Y., Takai Y.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
                                                                                                                                                                                                                                                                                                                                        SUBDNIT NRZB.
-!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 GUANYLAFF KINASE-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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                         Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDI 93
                                                                                                                                               Mueller B.M., Kistner U., Kindler S., Chung W.J., Kuhlendahl S., Fenster S.D., Lau L.-F., Veh R.W., Huganir R.L., Gundelfinger E.D.,
                                                                                                                                                                                                  "SAP102, a novel postsynaptic protein that interacts with NMDA receptor complexes in vivo."; Neuron 17:255-265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.7%; Score 90; DB 1; Length 849;
Best Local Similarity 20.5%; Pred. No. 2.7;
Matches 31; Conservative 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN SHORT ISOFORM).
34DA9C46C7BB96DB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; 1PR001478; PD2.
INTERPRO; 1PR001478; PD2.
INTERPRO; 1PR001478; PD2.
INTERPRO; 1PR001452; SH3.
Pfam; PF00018; SH3; 1.
Pfam; PF00055; PD2; 3.
Pr000m; PD000066; SH3; 1.
SMART; SM00072; GuRC; 1.
SMART; SM00028; PD2; 3.
SMART; SM00326; SH3; 1.
PROSITE; PS00025; GUANYLATE_KINASE_1; 1.
PROSITE; PS50002; GGANYLATE_KINASE_1; 1.
PROSITE; PS50002; GGANYLATE_KINASE_2; 1.
PROSITE; PS50002; SH3; 1.
SH3 domain; Repeat; Alternative splicing.
DOMAIN 149 335 PD2 1.
DOMAIN 244 330 PD2 2.
DOMAIN 404 484 PDZ 3.
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                                                                                                                                  MEDLINE-96374358; PubMed-8780649;
                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                  SEQUENCE FROM N.A. (LONG FORM).
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              Rattus norvegicus (Rat).
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849
640
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849 AA;
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Db 813 FTAIVQG-DSLEEIYNKIKQIIEDQSGHYIW 842
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Search completed: January 22, 2003, 08:53:39 Job time: 8.97715 secs

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January 22, 2003, 08:49:36 ; Search time 27.9086 Seconds (without alignments) 1321.544 Million cell updates/sec
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                                                                                                                                                             US-09-767-215-2_COPY_826_1004
930
1 RPRPVLLVPRAVGKILSEKL.....VRQAIADEQKKVVWTEQSPR 179
                                                                                                                                                                                                                                                                                                                   671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_organelle:*
sp_phage:*
sp_plant:*
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2: sp_bacteria:*
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6:
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Maximum DB s
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	Description	O8tes3 homo sapien	homo	Q8tdm7 homo sapien	Q8tdm6 homo sapien	Ogue73 homo sapien	Q9d3x0 mus musculu	Q96in2 homo sapien	Q960n4 drosophila	Q94880 drosophila	Q9vhk4 drosophila	Q9vkq8 drosophila	097758 canis famil	P70625 rattus norv	Q20398 caenorhabdi	09vtb3 drosophila	Q9w7fl brachydanio
SUMMARIES	ID	Q8TES3	Q9Y4E3	Q8TDM7	Q8TDM6	Q9UE73	Q9D3X0	Q961N2	Q960N4	094880	Q9VHK4	Q9VKG8	097758	P70625	020398	Q9VTB3	Q9W7F1
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	% Query Match Length DB	1171	1281	1809	1809	674	262	185	974	1367	1445	1916	1769	813	1034	233	576
	% Ouery Match	26.1	14.0	14.0	14.0	13.8	13.6	12.2	11.9	11.9	11.9	11.4	10.8	10.7	10.2	9.9	9,5
	Score	242.5	130.5	130.5	130.5	128.5	126.5	113.5	110.5	110.5	110.5	106	100.5	99.5	94.5	92.5	88.5
	Result No.		7	m	4	S	9	7	ထ	6	10	11	12	13	14	15	16

07 07 07 08

094hv2 gallus gall 09d647 mus musculu 09d478 mus musculu 09ndd3 trichinella 09nd3 trichinella 09hv12 drosophila 09hv13 mus musculu 09gy96 leishmania 081015 arabidopsis 09bv7 homo sapien 015424 homo sapien 015424 homo sapien 015424 homo sapien 015424 homo sapien 09c84 mus musculu 08wt18 drosophila 09vh16 drosophila 09vh16 drosophila 09vh16 drosophila 09vh16 drosophila 09fy33 sulfolobus 09c104 homo sapien 09c284 mus musculu 06c2402 mus musculu 06c402 mus musculu 062402 mus musculu 062337 tupaia glis 095337 tupaia glis 095337 tupaia glis 095338 tupaia glis	T; 1171 AA.  ted) sequence update) annotation update) aniata; Vertebrata; Euteleostomi; tarrhini; Hominidae, Homo.  Okumura K.; ng cDNA clone isolated from human /GenBank/DDBJ databases.  FA567ABBC8A703FF CRC64; re 242.5; DB 4; Length 1171; d. No. 7.6e-14; Mismatches 76; Indels 7; Gaps 4; -FKKCLAFYLSQEEYEAMSQRGDIIOEGEVS 55	SEKNPN 1
3 13 Q9YHV2 2 11 Q9D647 2 10 Q9D6478 7 Q9D023 8 5 Q9VNL2 1 Q9GV96 1 Q9GV96 1 Q9GV87 9 Q9GV87 9 Q9GV87 1 Q9GV84 3 Q9WT18 3 Q9WL6 3 Q9WT18 3 Q9WL6 3 Q9WT18 3 Q9WL6 3 Q9WT18 3 Q9WL6 3 Q9WT18 4 Q9UL64 3 Q9WT18 4 Q9GV23 6 Q9GV33 7 Q9ST38 6 Q9GU3 7 Q9ST38 7 Q Q9ST38 7 Q Q9ST38 7 Q Q9ST38 7 Q Q9GT03 7 Q Q9ST38 7 Q Q9GT03 7 Q Q9GT03 7 Q Q9GT03 8 Q9GT0	· eo Lo ar tta x	SELLINSGAMEFTICKSDIVT
88 9.5 1163 847.5 9.4 5867.5 9.4	PRELIMII 583; 700-2002 (TrEMBL.)	. 0
11112222222222222222222222222222222222	RESULT 1 Q8TES3 AC Q8TES3 AC Q8TES3 DT 01-JUN	o da

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Q8TDM6
           Q8TDM7
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                                                                                                                                                                                                                                                                                                                                                                                                                             153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TDM6
28TDM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
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                        δλ
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                                                                                                                                                                                                                                                                                                 Array Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can recomplete sequences of 100 new cDNA clones from brain which can recomplete sequences of 100 new cDNA clones from brain which can recomplete sequences of 100 new cDNA clones from brain which can recomplete sequences of 100 new cDNA clones from brain which can be recompleted by the recomplete sequences.

The INTERNATY: CONTAINS 1 SH3 DOMAIN.

BY INTERPOOR INTERNATY: CONTAINS 1 SH3.

THEAPTO: IPRO00408; RBG. Chr.condens.

BY Fam; PRO0525; Guanylate_kin; 1.

BY RAMAT; SM000728; PDZ; 4.

BY RAMAT; SM000228; PDZ; 4.

BY RAMAT; SM000228; PDZ; 4.

BY RAMAT; SM000228; CALL 2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                    MEDLINE-98290545; PubMed-9628581;
Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RPVL-------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD
                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.0%; Score 130.5; DB 4; Length 1281; Best Local Similarity 26.7%; Pred. No. 0.0021; Matches 55; Conservative 31; Mismatches 63; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 1 1
SEQUENCE 1281 AA; 140286 MW; 4CC150D03F3ED8B9 CRC64;
                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                 1281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                         Created)
                                                                                                                                                       KIAA0583 protein (Fragment).
KIAA0583.
                                                                                                                         01-NOV-1999 (TrEMBLrel. 12,
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                            TISSUE-BRAIN
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                                     1168 E 1168
               176 9 176
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Q9Y4E3
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RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1630 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF-----VDYKRR 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RPVL-----LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 1809;
                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Shah G., Brugada R., Roberts R.;
"Complete cloning and genetic organization of KIAA0583.";
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352033; AAL8397.1; "SEQUENCE 1809 AA: 202039 MW; 4794A6C8561CD905 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shah G., Brugada R., Roberts R.;
"Complete CDNA of KIAA0583/DLG5.";
Submitted (FEB-2201) to the EMBL/GenBank/DDBJ databases.
EMBL, AF322034; AALB3938.1; --
SEQUENCE 1809 AA: 202066 MW; 3B77B3DCAD6FD6E9 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 130.5; DB 4; 26.7%; Pred. No. 0.0032; Live 31; Mismatches 63;
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1809 AA
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                             Q8TDM7;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.7%
Matches 55; Conservative
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  PRELIMINARY;
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Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
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      QQ
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Nakamura H., Sudo T., Tsulki H., Miyake H., Morisaki T., Sasaki J., Masuko N., Kochi M., Ushio Y., Saya H.; "Identification of a novel human homolog of the Drosophila dlg, P-dlg, specifically expressed in the gland tissues and interacting with p55.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 RPVLILGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF-----VDYKRR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSV 102
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                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (Hrman).
01-JUN-2002 (Human).
02-JUN-2002 (Human).
03-JUN-2002 (Human).
03-JUN-2002 (Human).
03-JUN-2002 (Human).
04-JUN-2002 (Human).
04-JUN-2002 (Human).
04-JUN-2002 (Human).
05-JUN-2002 (Human).
06-JUN-2002 (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            674 AA; 74892 MW; C4C006B0A4F7E8E8 CRC64;
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26.7%; Pred. No. 0.0015;
ive 30; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00018; SH2; 1.
SMART; SM00072 GuKc; 1.
SMART; SM000228; PDZ; 2.
SMART; SM00326; SH3; 1.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 433:63-67(1998).
-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL: 001043; AAC61295.1; -.
HSSP: Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PDZ.
InterPro; IPR000408; Reg_chr_condens.
InterPro; IPR001452; SH3.
                                                                                                                                                1783 LSSICTQILAMVNQEQNKVLWIPACP 1808
                                                                                       153 LDGLLSCVRQAIADEQKKVWTEQSP 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98409314; PubMed-9738934;
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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tes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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1D 09UE73
1D 09UE73
1D 01-M
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RESULT 6 Q9D3X0

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Carralmed Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ashaa M., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S., Arawai J., Saito T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rabil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Browstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., Brownstein M.J., Bult C., Romiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saraki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Wilming L., Washima Y., Kawaji H., Kohtsuki S., Anderia V., Kawaji H., Kohtsuki S., Anderia V., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | SGHFDV-----TTVASIKEITEKNRHCLLDIAPHAIERLHHMHIYPIVIF--1 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 NEKMAKKLK------KGLQRLGTSEEQLLEAARQEEGDLDRAPCLYSSLAPDGWSD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 RPVLLLGPLLDVVKEMLVNEAPGKFCRCPLEVMKASQQAIERGVKDCLF-----VDYKRR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RPVL------LVPRAVGK-----ILSEKLCLLQGFKKCLAEYLSQEEYEAW 42
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%; Score 126.5; DB 11; Length 262; 25.7%; Pred. No. 0.00075; Live 32; Mismatches 64; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).

EMBL; ARO16979; BAB30534.1; -
MGD; MG1:1918479; D163.

InterPro; IPR000619; Guanylate_kin.

Pfam; PF00625; Guanylate_kin; 1.

SMART: SM00072; GuKc; 1.

SMOSTIE: PS06052; GUANYLATE_KINASE_2; 1.

SEQUENCE 262 AA; 30033 MW; A2A5629478469514 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 19, Last sequence update) Similar to guanylate kinase 1 (Fragment). Homo sapiens (Human).
                                                                                        Last sequence update)
Last annotation update)
262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AA
                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 LDGLLSCVRQAIADEQKKVVWTEQSP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 LSSICTQILAMVSQEQSKVLWIPACP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                        01-JUN-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                   4933429D20Rik protein.
DLG5 OR 4933429D20RIK.
                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
                          29D3X0;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
0961N2
1D 0961N
AC 0961N
DT 01-DI
DT 01-DI
DE SIMI.
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SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                 PYD OR TAMOU OR CG9763.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahisa M., Togashi S., Suzuki T., Kobayashi M., Murayama A., Kondo K., Miyake T., Ueda R.; The Drosophila tamou gene, a component of the activating pathway of extramacrochaetae expression, encodes a protein homologous to mammalian cell-cell junction-associated protein 20-1."; EMBL, D83477; BAA11923.1; -.
---ATSGKCRIV 847
                            63 RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                 120 SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                          Length 1367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148347 MW; 571C4566C6B68BF8 CRC64;
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 110.5; DB 5; 23.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
 803 RPVVLF-GPVSDLARERLA--KDFPDKFSTPLQDDDKSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. SEQUENCE 1367 AA; 148347 MW; 571C456
                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flybase; FBGN000317; pyd.
Interpro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96312452; PubMed=8698238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00595; PDZ; 2. SMART; SM00072; Gukc; 1. SMART; SM00228; PDZ; 3. SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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02,
21,
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                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q12923; 3PDZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 KVVWTEQS 177
                                                                                                                                                                  953 GAVWMSES 960
                                                                                                                                         170 KVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CANTON-S
                                                                                                                                                                                                                                    Q94880
Q94880;
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PVD OR CG9763.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                               43 FVTREVMORDIAAGDFIEHAEFSGNLYGTSKVAVQAVQAMNRICVLDVDLQGVRNIKATD 102
                                                                                                                                                                                                                                                                                                                                               93 IFPIVIHVSVNEKMAKKLKKGLQRLGT-SEEQLLE--AARQEEGDLDRAPCLYSSLAPDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                                                                                                                                                                                                                                                          33 YLSQEEYEAWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 974;
                                                                                                                                                                                                                                      12.2%; Score 113.5; DB 4; Length 185; 26.2%; Pred. No. 0.0079; Live 36; Mismatches 61; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                       Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2001); -.
InterPro; IPR000619; Guanylate_kin.
Pfam; PF00025; Guanylate_kin.
PROSTITE; PS000856; GUANYLATE_KINNSE.
PROSTITE; PS50052; GUANYLATE_KINNSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5FA3A7D7D0922C2E CRC64;
                                                                                                                                                                                                     1
20646 MW; 3FF55B058C757184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.9%; Score 110.5; DB 5; Best Local Similarity 23.4%; Pred. No. 0.11; Matches 44; Conservative 37; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50052; GUANYLATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 3. SEQUENCE 974 Aa; 107338 MW; 5FA3A7D71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00625; Guanylate_kin; 1. Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                        160 -DSLDQAYAELKEALSEEIKK 179
                                                                                                                                                                                                                                                                                                                                                                                                       150 WSDLDGLLSCVRQAIADEQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                     Local Similarity 26.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                             185 AA;
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                                                              SEQUENCE FROM N.A.
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                                  NCBI_TaxID=9606;
                                                                             TISSUE-OVARY;
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SEQUENCE
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Matches
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RA Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. George R.A., Forder W. P., Sandell M.D., Zhang Q., Chen L.X.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Barlew R.M. Basu A. Baxendale J., Baytaktaroglu L., Beasley E.M.,
R. Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Dodgon K., Doup L.E., Downes M., Dugan-Rocha S., Pleischman W.,
R. Aberis M., Gabriellan A.E., Garg N.S., Gelbart W.M., Classer R.,
R. Godbriellan A.E., Gorrell J.H., Garlus P., Harrish M.,
Alush F., Karpen G.H., Ke Z., Gubar M.M., Chelson D.L.
R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R. Matteil B., McIntosh T.C., Morris J.M., Moller D.L.,
Mount S.M., May M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,
R. Markulov G. Mlishima N.V., Mobarry C., Morris J.M., Moller E., Shen H.,
Shue B.C., Siden K.Hamos I., Simpson M., Stupski M.P., Smith T.,
R. Spier E., Sparalling A.C., Staplecton M., Stupski M.P., Smith T.,
R. Wasaaman D.A., Walnston R.M., Worley C., Wu D., Yang S., Zhu O.,
R. Yen R. F., Zaverl J.S., Zhan M., Zhong G., Zhao Q., Zhao Q., Zhao G., Zhan R., The genome sequence of Drosophila melanogaster.",
R. Schence S. Brotter E., 184, 2019 S., 184, 201
                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                            PYD protein.

PYD OR CG9763.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Iracheata; Hexapoda; Insecta; Musor
                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                          PRT; 1445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00218; ZU5; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, Q12923; 3PDZ.
FlyBase; FBgn0003177; pyd.
InterPro; IPR000619; Gaanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
InterPro; IPR000906; 2U5.
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                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
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                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                              Q9VHK4;
                                          Q9VHK4
RESULT 10
                      09vнк4
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Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Adams M.D., Celliker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
R. Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Worthman J.R., Yandall M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Balazej R.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Ballew R.M., Carley S.W., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Bortova D., Botchan M.R., Dong Z., Mays A.D., Dew I., Dietz S.M.,
Borkova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A clerry J.M., Carley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Taris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R. Harris N.L., Harvey D., Heiman T.J., Wernandez J.R., Houck J.,
R. Harris N.L., Harvey D., Heiman T.J., Wennison J.A., Ketchum K.A.,
A Jalai M., Kalush F., Karpen G. H., Ke Z., Kennison J.A.,
R. Markei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
R. Markei B., McIntosh T.C., C., Scheeler F., Shen H.,
R. Raison D.R., Nixon K., Nuxon K., Nuxon D.,
R. Rainert K., Remighton K., Saunders R.D.C., Scheeler F., Shen H.,
R. Spier E., Spradling A.C., Standers R.D., Puri V., Raese M.G.,
R. Spier E., Spradling A.C., Standers R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                632 RPVVLF-GPVSDLARERLA--KDFPDKFSTPLQDDDKSA------ATSGKCRIV 676
                                                                                                                                                                                                                                                        RHA-VESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK-MAKKLKKGLQRLG-T 119
                                                                                                                                                                                                                                                                                                                                                 SEEQLLEAARQEEGDLDRAPCLYSSLAPDGW-----SDLDGLLSCVRQAIADEQK 169
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                   Gaps
                                                                                                                                                            3 RPVLLVPRAVGKILSEKLCLLQGFKKCLAEYLSQEEYEAWSQRGDIIQEGEVSGGRCWVT 62
                                                                                                                 43;
                                                                     Length 1445;
                                                                                                                 Indels
PROSITE; PS50106; PD2; 6.
SEQUENCE 1445 AA; 156723 MW; A5675FB66676A40E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG6509 protein (LD32687p).
                                                                                                              64;
                                                                     DB 5;
                                                                   11.9%; Score 110.5; Di
23.4%; Pred. No. 0.18;
ive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                  Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      782 GAVWMSES 789
                                                                                                                                                                                                                                                                                                                                                                                                                                          170 KVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VKG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
Q9VKG8
                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                               δ
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InterPro; IPR000619; Guanylate_kin. InterPro; IPR001478; PDZ. InterPro; IPR001452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P70625
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P70625
    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BREED: COCKER SPANIEL;
MEDLINE=99196918; PubMed=10094817;
Gonzalez-Mariscal L., Islas S., Contreras R.G., Garcia-Villegas M.R.,
Betanzos A., Vega J., Diaz-Quinonez A., Martin-Orozco N.,
Ortiz-Navarrete V., Cereijido M., Valdes J.;
"Molecular characterization of the tight junction protein ZO-1 in MDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: : | |: | |: | |: | |- |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- ||
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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 MAKKLKKGLQRLGTSE-----EQLLEAARQEEGDLDRAPCLYSSLAPDGWSDLDGLLSC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 RPVLLVPRAVGKILSE-------KLCLLQGF---KKCLAEYLSQEEYEAWSQR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnívora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1916 AA; 209863 MW; 32B2A61ABA6848F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 106; DB 5
22.7%; Pred. No. 0.65;
iive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1769 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PDZ; 4.
                                                                                                                                                                                                                                                                                                                                                                                            FIYBASE: FBR00032363; CG6509.
InterPro: IRR000619; Guanylate_Kin.
InterPro: IRR001478; PDZ.
InterPro: IRR001478; PDZ.
InterPro: IRR001472; SH3.
Pfam: PF00555; PDZ: 3.
SMART: SM00278; GUC; 1.
SMART: SM00228; PDZ; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 VRQAIADEQKKVVWTEQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZO1-MDCK.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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097758
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STRAIN-WISTAR-KYOTO;
STRAIN-WISTAR-KYOTO;
MEDLINE-20027749; PubMed=10559001;
Adams L.D., Lemire J.M., Schwartz S.M.;
"A systematic analysis of 40 random genes in cultured vascular smooth muscle subtypes reveals a heterogenelity of gene expression and identifies the tight junction gene zonula occludens 2 as a marker of epithelioid 'pup' smooth muscle cells and a participant in carotid neointimal formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LHRMDIFPIVIHVSVNEKMAKKL------KKGLQRLGTSEEQLLEAARQEEGDLDRA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 EYLSQEE---YE-AWSQRGDIIQEGEVSGGRCWVTRHAVESLMEKNTHALLDVQLDSVCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;
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-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U75916; AAB46979.1; -.
HSSP; P31016; 1BE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P70625; P97625;
01.FEB-1997 (TrEMBLrel. 02, Created)
01.JUN-2002 (TrEMBLrel. 05, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 10.8%; Score 100.5; DB 6; Best Local Similarity 24.1%; Pred. No. 1.9; Matches 38; Conservative 35; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 PCLYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVWTEQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zonula occludens 2 protein (Fragment).
     -i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U55935; AAD11529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50052; GUANYLATE_KINASE_2; PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                             InterPro; IPR000619; Guanylate_kin
                                                                                                                                     InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR000906; ZU5.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00018; SH3; 1.
Pfam; PF00791; ZU5; 1.
Exp. Cell Res. 248:97-109(1999).
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01597; ZONOCCLUDNS.
PRINTS; PR01598 ZONOCCLUDNS1.
PRINTS; PR01600; ZONOCCLUDNS3.
SMART; SM00072; GUKC; 1.
SMART; SM00228; PDZ, 3.
SMART; SM00326; SH3; 1.
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STRAIN-BERKELEY;
                                                                                                                                                                                                                              1025 VWVQR 1029
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                                                                                                                                                                                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 EKVLLREAGFKKPVVLFGPIADIAMERLT -- TELPDLFQTAKTEPKDAGSEKSSG -- VVR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 RHAVESLMEKNTHALLDVQLDSVCTLHRMDIFPIVIHVSVNEKMAKKLKKGLQRLGTSEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 QLLEAARQ--EEGDLDRAPC-----LYSSLAPDGWSDLDGLLSCVRQAIADEQKKVVW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                          18 EKLCLLQ-GFKKCLAEY----LSQEEYEAWSQRGDIIQE-----GEVSGGRCWVT
                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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                                                                                                                                                                                                                                                                                                                           Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116053 MW; 7E29646264FCD5BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                          813 AA; 90776 MW; 30EA78F19DE9C852 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                         Score 99.5; DB Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1034 AA.
                                                                                                                                                                                                                                                                                                                                                                   38; Mismatches
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PD2; 1.
Pfam; PF0018; SH3; 1.
PRINTS; PR01597; ZONOCCLUDNS.
PRINTS; PR0072; GUANC; 1.
SMART; SM000226; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50025; GUANYLATE_KINASE_2; 1.
PROSITE; PS500105; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
PROSITE; PS50106; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Sclence 282:2012-2018(1998).
EMBL, 268298; CAA92607.1;
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
SWART; SM00072; GuKc; 1.
SWART; SM000728; PDZ.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                           10.7%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                     43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE · 1034 AA;
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         SH3 domain.
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020398
020398
AC 02039
AC 02039
DT 01-NO
DT 01-DE
DE F44D1
OS Caeno
OC Rhabd
OC Rhabd
OC RNB [1]
RN SEQUE
RN SEQUE
RN GEOUS
RN SMART
DR SMART
DR SMART
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Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ARC03547; AAF501391; --
EMBL, AV071035; AAL48657.1; --
HSSP; P15454; LGKY.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.9%; Score 92.5; DB 5; Length 233; Best Local Similarity 22.6%; Pred. No. 0.94; Matches 45; Conservative 32; Mismatches 81; Indels 41
                                                                                                                                                                                                        Masse; Figh 100036099; CG11811.
InterPro; IPR002198; ADH_short.
InterPro; IPR00619; Quanylate_kin.
Pfam; PF00625; Quanylate_kin.
Pfam; PF00625; Guanylate_kin.
PROMITS; RONO072; Gukc; 1.
SMART; SM00072; Gukc; 1.
PROSITE; PS00866; GUANYLATE_KINASE_1; 1.
PROSITE; PS00856; GUANYLATE_KINASE_2; 1.
SEQUENCE 233 AA; 25898 MW; 12C4C5CC715C2885 CRC64;
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